

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCACCAAGGCCTCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAATCTAAAGAGGCAGCATTTGGAACCATCGATGGAAAAATATTTTAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCTATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCTCTCCACTGTGCCCATGTGTGCCCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGGCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAACTCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**G**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAATATCTTTGTTTAAATGGGGCAGATATGC
 ATTTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAAACATAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAAACAAGTGGTCATTGTACATTCATTT
 GCTGAACCTTAACAAAACCTGTTTCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACATATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCAG
 AATACAAACAGTATACTCATG

09-10-2008 09:20:20

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWVFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLS IYMDTLNIFMRVATMLATGGNRKK

0947322-00004

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCTCCGCCCTTCTGCAT
 CGCGGCTTCGGCGGGCTTCCACCTAGACACCTTAACAGTTCGCGGAGCCGGCCGCGTCTGTGAGG
 GGTTCGGCACGGGGAGTCGGGCGGTCTTGTGCACTTTGGCTACCTGTGGGTCCGAAC**ATG**TCGG
 ACATTCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGGCTATTGGTTCGCCGCCACCTTCG
 CGCGTGCCTTGGTTCGGCAAACTTCGGGCTCATCAGCCCGGCCCTACCTTCTCCTCTCGGCCCA
 AGCCTTCCTTTATCGCTTTTTCAGATTTCGAGGGCCAATCAGTCCCACTTTTATTTCCCTGTGG
 GTCCAGGAACCTGGATTTCCTTATTTGGTCAATTTATATTTCTATATACGATTCTTACGCGA
 CTTTGAAACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTAACTG
 GATTTCGATCGTGATTACTGGCTTAGCAATGGATATGCACTTGGCTGATGATTCTCTGTGCA
 TGTCACTACTTTATGTCTGGGCCAGCTGAACAGACATGATTGTATCATTTTGGTTCGCA
 ACACGATTAAAGGCTTGCTATTTACCTTGGGTTATCCTTGGATTCACTATATCATCTCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTATTTTTCCTAATGTTCA
 GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGGATATCAGGATTGGTGTGCCCTCTAGCATAGCGCGAGG
 TGTGTATCAGAAATGGCGGAGGCGGGAGACAACTGGGGCCAGGGCTTTCAGATTTCGAGACC
 AG**TGA**AGGGGCGGCTTCGGGCGAGCGCTCCTCTCAAGCCACATTTCTCCTCCAGTCTGGGTG
 CACTTAAACAACTCGCTTCTGGCTAACACTGTTCGACCTGACCCACACTGATGTAGTCTTTT
 AGTACGACCAAAAGTTTCTTAAATCCCGAAGAAAATATAAGTGTTCACCAAGTTTTCAGAT
 TCTCATTTCAAGTCTTACTGCTGTGAAGAACAATACCAACTGTGCAAAATGCAAACTGAC
 TACATTTTTTGGTGCTCTCTCTTCTCCCTTTCCGCTCTGAATAAIGGGTTTTAGCGGGCTT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGCACACATGCCCTCTCCTCCACTTTTCCCAACCCCACTTTGCAACTAGAAAAAGTTG
 CCCATAAAATTTGCTCTGCGCTTGACAGGTTCGTATTTATTTGACTTTTGCCAAAGCTGTGTC
 ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCAGATGACATCCGTCTT
 AACCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAGTACCACTGAGTTCATGAGGCCA
 CAGATTGGTTATTAATGAGATACGAGGGTGGTGCTGGGTCTTTTCTTCTCAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACATGGGGAGTCAACCCC
 TTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTGATGCTGAGTAGTGTGGTTTGTGTGT
 TAGGAGGATCCAGATCATGTGGCTACAGGGAGATGCTCTTTTGGAGAGGCTCTGGGCAATG
 ATTGCCATTTCAATCTCATTTGGATATGTCCTTATTTAGTAAAGAGGAGAGACCTCATAT
 CGCTATTTAAATCTACTTTTTCCTATCCCTGTTTGGTTCATGTTTCAATTAATGT
 GAGGAAGCGGAGCTCTCTCTGACAGTATGATTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTAAAGCTTGAATGGCTTTAGAATCATTTGGGTTTGAAGGTTGTGTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACAGCTTAAATACCAACCTTTTTT
 TCGTAGGTCGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTGAAGGCCA
 TGGCTTTTACACAGATTATTTATTTATGACGTTATCTGAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGCTGTCACTTTGAGGCAACTAAAAAGGCTTCAACAGTTTTGATCAGTTTCTT
 TTCAGGAACAATTGTGCTCTTAACGATGACATTTCTTTCCCACTCTTAAACAGTGTGAT
 GTGTCTTATCCTAGGAATGAGAGTTGGCAACAACCTTCTCATTTTGAATGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGTCTGAACCTTAAGTGTG
 TGTTTGTGTTCATCTGTGGCCCAATAAAGTTTACTTGTAAATTTAGAGGCCATTA
 CCAATTTAGTTCAGCTGACTCATTTGTACAGCGTGGAGACTCATTTGATGTATAAGATA
 TTTCTGACAGTGAGTACCCGGAGTCTCTGGTGTACCTCTTACAGTCAAGTCTGCGGAG
 CAGTCATTTTTCCTAAAGCTTTACAAGTATTTAGAAGCTTTGACTTCAGGCAAAATGTT
 ATGAAGTTTATCTCTTAAACATGGTTAGGAAGCTGATGACGTTTATGATTTGTCTGGATT
 ATGTTCTTGGAAATAATTTACCAAAACAGCTATTTTGGTTCAGTTGACAGGCAAAACA
 TGACAGTGGATTCTTTACAAATGAAAAAATAATCCTTATTTGTATAAAGGACTTCCC
 TTTTGTAACTAATCCTTTTTATTGGTAAAAATGTAAATTAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
STAGCTTCTATCTTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGT
CCTTGTGCCCCAAAGGCTTAACCGGGGTCGCGCGGTCTGGCCTAGGGATCTTCCCCTGGCC
CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGTTGATTTTGGT
GGCCTGTGTTCCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACAAGTGTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTTGGAAT
AATGAAGATCAATTTCAAGAAGCATGCATTTCTCTTCGAAAGACCCATACATCAGAGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGTGTCAGA
AAAACATTGAAATGCAGCTGCAAGCCATTGAAATTAATTCAGAGAGAAATGGTGTATTACCT
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAACAGAAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
TGCTAATCAGTCAATAGAACCCTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCCTCCCTCC
CACAAAAAGGCCCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
TTATCAGTACTTGGAACAGAGAACAATTCGGCAACGAGAAACATATCTCAAGCAGAAGAGAGA
TAAGTTGATGCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAG
CAACATTAATAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAGCTA
ATAATTAGAACAATTTAACAAAATGGAAGTTCAAATTTGCTTTAAAAATAAATTTATTAGTC
CTTACACTG

FIGURE 6

MAEEEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQYKELVEKLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLA AEDFTIFKAMMVQKN IEMQLQAIRIIQERNGLVPDCLTDGSDVVS DLEHEEMKILREVL
RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGP IANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRL LAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGATT
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
CCTGAGGGAAGTTCTTAGAAAAATCAAAGAGGAATATGACCAGGAA

094109-00001

FIGURE 8

CGTGGTTTTTGTTCCTCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
TAGCTTCTCCAGGTATGGACCCCTAAGGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGCT
TCTCAGCTCTAGAGTATGTCGCTTCTTCCACTAGAAGCTCTCTCGAGGAGGTAATAAAAAAC
AGTGGAAATGGAAGAAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTGTGCAACAATGTATAC
ATTCCTGCTAGAGTGCCATATTCATGTTCTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
TCGCCAATGAAGAAACAAAGTATGATTATCTTCCAACACTACTGTGAATGTGTCTCAGAAGT
GTGAAGCTAGTTTCTGTGTGCTTGTGTATTCTGTGTTATAAAGAAAGATCATCAAGAGTAG
AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATCTCTGCCT
TCTTTATTCTTCCGGATAACTTGATTGCTCTTCTATGCTGCTCTATCTTCAACAGCAAT
GCTGTATCTTCTCAAAATTTAGCATATTAACAACAGCTCTTCTATCAGGATAGTGTCTGAA
AGGCGCTCTAACTGGATCCAGTGGCTTCCCTCTGACTTTATTTTTGCTATTGTGGCT
TGACTGCGGGGACTAAAACTTTACAGCAACAATTTGGCAGGACGTGGATTTCATCAGCATGCC
TTTTTCAGCCCTTCCAATTCCTGCTTCTTTTCAAGAAGTGAAGTGTCCCGAAGAAAGCAATTTG
TACAGAAAGGAATGGACTTTTCTTGAAGCTAAATGGAACACACAGCAGAGTTTTCAGTC
ACATCCGTCCTGGCATGGCCATGTTCTTATTATAGTCCAGTGTTTATTTCCTCAATGGCT
AATATCTAATGAAGAATAGTACTGAAGGAGGGGAACAGCTACTGAAGACATCTTCATACA
GAACAGCAAACTCATTTTCTTGGCATCTGTTTAAATGGGCTGACTCTGGGCTCTCAGAGA
GTAACCGTGATCAGATTAGAAGATCTGGATTTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTGAATATGCATTCAGGCGCTTTTCAGTGGCTTTCATTCTGAAGTCTCGGATA
CATGTTCCATGTCCTGATGGCCAGGTTACCAGTGTCAATTACACAACAGTGTGTGCTCGG
TCTTTGACTCTCAGGCGCTCCCTGGAATTTTTCTTGAAGCCCATCAGTCTCTCTCTATA
TTTTATTATAATGGCCAGCAAGCTCAAGTTCCGGAATACGCACCTAGGACGAAGAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTT
CAACCAACCAAGAGTGATGAGTCAGATGAAGATACCTTTAACTGGTACCACATAGTTTCCA
GCTCTCTTGAACCTTATTTTACATTTTTCAGTGTTTGAATTTTATCTTTTCATCTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTCTTGCATATATCTAGCTACTCCCTAAATGGTT
CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAATATCTAAGAAAGCTGATACAGGAGTAACA
ATATGAAGAATTCATTAATATCTCAGTACATGTATAATCAAGAAATTAATGTGCAGATTAT
TTTCCTTGCCCTTCAAGCTTCCAAAAAATCTGTAATATCATGTAGCTATAGCTTGTATAT
ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTAGTTTACATGCCAAAGT
CTCTCTCTTTTAACTATATAAAGCTAGGTTGTCTCTGAATTTTGAAGCCCTAGAGATAGT
CATTTTGAAGTAAAGAGCAACGGGACCCCTTCTTAAAACAGTGGTTTGAAGGACCTAAATAT
CTGGCCATACCATAGATTTGGGATGTAGTCTGTGCTGCTAAATTTTGTGGAAGAACAGT
TTCCTCAGACAACAACCTCAGAAATTTTAAATTTTGAATTCATGGGAAATTTGGATTTTGT
AATATCTTTTGTGATTTTAAACATTTGGTTCCCTAGTACCATTAGTACCACTGTTATTTTA
AGACTTTTAAACAGGACCGGTGGGGGCTTTTTTCTCTCAGTTTGAAGAGAAAACTTCGAT
GTCATTACTCCTGAATATTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACT
AATTCAGCTGTGACTATTTGATATCTTCCAAGAGTTGAATTTCTGCTGCTTCAGATCATAC
CAGATTTGTGAGTGAAGTCATGTGCTTGAAGACTTTTAAAGGATCCTTTCAAAGGATCACTT
AGCAACACATATTTGACTTTTAACTGATGTGAATATTAATCTCTTAAAGATAAGAAAGTACG
AGTAATATATAAGTCACTTTACAGTGCTACTTCAACATTAAGCTGAATGGTATTTTACG
GATTTTTGCATCGAGCCAGTTAACTCTGTFAGTAGAGAAGTCAGGTGATAGATGATATTAA
AAATAGCAACAAAAAGTGACTTGTCTCAGGGTCTACGAGCTGGGTGATGATAGAAGAGTGG
CTTTAACTGGCAGCGCTGATGTTTACAGACTACCATGTAATCTGAATATGAGCTTTATGGTGT
CATTTCTCAGAAACCTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCGAGTGAATATA
AGGTAATATATCATATATAATCATTTTGTATGCCAATAATATGACTGGCAAGAATTG
GTGGAATTTTGTAAATTAATAATTAATAACCT

FIGURE 9

MEKQCCSHFVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDFF
SPNSCCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESEDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAAGAGGCGCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGCCTTGACTGCCGGGA
CTAAAACTTTA

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGC
TGGTCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTCGGGGACGAGGAGCAT
CCGCTCTACAGGTCCCAAGCGGCTGGCCCGGGGTATGCCCAAGGAAGCGCCGAG
AGCGGCTCCGCGCGGGGCTGCTACCCACGAGCTCTTCAAAGCACTGAACGCCCGGCGTAA
GGTAGAAGAAGAACGAAAAGAAAGAAACAAGTTGCTGTCTTGGCAAGACTTTGCTATG
CACTTGGGGGAGCCCCACAGGTGTACGGGCTGTGCCCTGGGTTTCTTCCTCAGATCTAG
CTATTG**ATG**TGGCTCAGGTGGGCCCTTTCTGCTCCATCATCTGTTTGTGGGCGGAGC
TGGGATGCCATCAGACACCCCTGTGGGCTCTGCATCAGAAATCCCTCGACCTGCC
TGGGTGCGCTTAGTGCCCTGGATCATCTTCTCCACGGCCCTGGCGCTATTGCCTACTTCTC
ATCTGTTCTGTGCGGCACTCCCAACGGCGAGCACTTGTAGTACTGCTTTTCTATTGGCT
CTTTGAAACAATGGTCACGTTGTTTCCATGTTCCCTACTCGGCTCTACCAATTTCTCATCAGA
ACCGAGCAGACTGAGCGGATTTCTGCCACGCGCTATCGGATGACTGTGAGCATGCTGGGCA
AGTCTGGGACGGCGATCCAGGGAACAATCGTGGGCAAGCAGACGCTTGTTCACGAG
ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACATAGGCACCACTCACAG
AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGCTGTATCTATATAATCTG
TGCTGTATCTGTATCTGGGCTGCGGGAGCAGAGAAACCTATGAAGCCACGAGCTGTG
AGCCAATCGGCTACTTCCGGGGCTACGGCTGGTCTGAGCCACGGGCCATACATCAAATT
ATTACTGGCTTCTCTTCACTCTCTTGGCTTTTCATGCTGGTGAGGGGAATTTGCTTGTGT
TTGCACTACACCTTGGGCTTCGCGAATGAATTCAGAACTACTCTGGCCATCGCTCT
CGGCCACTTTAACCATTTCCCATCTGCGAGTGGGTTCTTGACCGGTTTGGCAAGACAGCT
GTATATGTTGGGATCTCATCAGCATGCCATTTCTCATCTTGGTGGCCCTCATGGAGATTA
CCTCATATTACATATCGGTTAGCTGTGGCAGCTGGCATCAGTGTGCGAGCTGCTCTTTAC
TGAACCTGGTCTCATGTGCTGTATGTATTGACGACTTCCATCTGAAGCAGCCCACTTCAT
GACCACGAGCCCATCTTCTTCTCTTCTATGTTCTTCTTCAACAGTTTGCCTTGGAGTGTC
ACTGGGCATTTCTACCCCTCAGCTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC
CGGAACGCTGTCAAGTTTACATGAACTAGCTGTGACATAGGCTCCATAGTTTCTATCCCTG
CTGGGCTGCTGCTCTTCAAATGTACCCCATGATGAGGAGAGGCGGCGCAGATAAGAA
GGCCCTGACGGCACTGAGGGACGAGGCGACGAGCTTGCTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGCTAGGACTCTCT**TAG**GGCCCGCCACGTTGCCCGAAGCCACATGCAAGAGGCCACAG
AAGGATCAGCACTGTCTGCCGGCTTGTGTAGACAGCTGGACTGCAGGTGCTAGGAAGGAA
CTGAAGACTCAAGAGGATGTGGCCGAGACACTTGTGTGCTCACTGTGGGCGCGGCTGCTGTG
TGGCCTCTGGCTCCCTCTGCTGCTGTGGTGGCAAGCCCTGGGCTGCCATCTGTAATA
TGCCAAGGACTGATCGGGCTTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
TAATTAATAACTTAATGACTGTGATCATAGCAATGTGTGTATGTATGTATGTCTGTGAGCTA
TTAATGTTTAATTAATTTTCAATAAAGCTGGAAAGC

FIGURE 12

MWLRWALS LPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQQGQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLFTSLAFMLVEGNFVLFCF
YTLGFRNEFQNL LLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLG LLLFKMYPIDERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

00445003002

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGCTCTGAAGACTAACATTTTGTGAAGTTGTAACACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTATGTTCTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAAACAAGGCTGGCCTTGTACTTGGAATACTGAGTTGTTTAGG
 ACTTTCATTGTGGCAAACCTCCAGAAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTG
 CACCTTGCCCTATTAAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCCTTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAGAAGCCATTTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACCTATGCCTATACTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAAFIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQM QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTA AEWSMSFSF GFFLT YIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

0304392-03281

FIGURE 17

CCCACGCGTCCGCCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGAC**ATG**CGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCGGGCTGCAC
 CTTGCGCTTGTA^{CT}TGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTC^{CT}CCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCC^{CT}ACGTGTTCCTGCTCTTCTGCGGCGCCTA
 CCTCTACAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAACAGTTGGTGGTGCCTACTTTCTGATAAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCCATGACACCAA^{CT}GGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCA^{GT}TCTTCTCTCAGTCTTATCGGTTTGATCCCATATAATTTCTCTGTGT
 GCAGACAGGGTCCATCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCTGGGACACTG
 TCTTTAAGCTGTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAAGA
 CACA**TGA**TCTGGATTTTCTGTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCTGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNLVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPFDKVALLRKVEENRNSLFFFLFLRLFPMPNPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCGCATGAATCATGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTTGGGATTTTATATTTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAATTTATCAGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTGAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLEDA PRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFV
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHQCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

bioRxiv preprint doi: <https://doi.org/10.1101/2020.03.10.332000>; this version posted March 10, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAACAGCCAGCTCAGAAATAGGAAAAATACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG
ATTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAAGAAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACCTGGTGGCAGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCCTGGCACCCCAATGGCCAGCCACCTTCTTTGAAGACTTCCAGGCTTTTGTGCCA
 CACCCGAATGGCCGCACTTCATCGACAAACAGGTACAGCCAACCTATCTCCAGTTCGAAATG
 GACACGTATGCTTAAGAGCCAGACCTTATGTACAGTTCTTGGAAATGCTGCTATGACATGCT
 TATGAGCAGTGGGCAGCGGCGCCAGTGGGAGCGCGCCAGAGTGTCTGCGGCTTCCAGGAGC
 TGGTGCTGGAACTTGGCGAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGGCGCTGTGGCCGAGCT
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACCTGCCA
 GCGCCGAGACATATTCACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
 CTCACCTGCTTGGCAGTGACCAAGAGGGCAAGTGAAGCAGCCACCCAGTTCGCTGCAGG
 AGGACAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCAGCAGAATG
 GATGAGCAGCGTGAAGAAGCTGGTGTGTGCGCCGAGTGCAGCTGTGTACGCTAGTGGCCGT
 GGTGCCAGGGCTGCTGGAGGTACCCACACAGAATGATACTTACGATGGCAGCACTGAGC
 GCTGGGAACCCGAGGAGGCGATCGGCTATGATTTCCGGCGCCACTGGCCGAGCTGGCTGAG
 GTCCACCTGCGGCGTTTCAACTGCGCCGTTACAGCACTTGAGCTCTTCTTTATCGATCAGGC
 CAACTCTCTCTCACTTCCCATGCAAGGTTGGGCGACGCCAGTCTCATCTCTAGCCAGA
 CTCGAGACCCAGCGTGGCCCATCCACCCCATACCCAGGTACGGAACCAAGGTGTACTCG
 TGGCTCTGCGGCTACGGGCCCTCTCAAGGCTACCTTAAGAGCCGCTCCCCAGAGAT
 GTGCTGTGCTCAGGCTTACCCAGAATGGGTACAGCTGAGATATPCCAACTTCGAGTCT
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTC
 CCTGGGCTCTGACAGCACTAGCTGTCTCCCAACCTTGGACCTCAAGCAACCGAGGCTCTTCG
 GGACCTGTCTAAGCCCATCGGTGTGTGAAGCCAGCATGCCAGCTGTGAGGGAGAAT
 ATGAAGCTTTGAGGACCGACAGGACGACATTGACAAGTTCCACTATGGCACCCACTCTCC
 AATGCAGCAGGCGTGATGCACTACTCTATCGCGCTGGAGCCCTTCACTCCTGCACGTCCA
 GTGCAAGTGGCCGCTTGTACTGCTCGGACCGGCACTTCCACTGGTGGCGGCGAGCTGCG
 AGGCAGCGCTGGAGACCCCTTGTACTGCTCGGACGAGTCTATCCGGAATCTTCTACTTTCTC
 GACTTCTGTGAGTACCAAGACGAGTGGTCTCTCTGAGACTTATCCAGCAGCAGCCGCG
 AGGCGATGTGAGTTCGAGTATGTCTTGCACACCTACACGAGTGGATGCACCTCATCTTTGGC
 TACAGAGCAGCGGGGCGAGCGGAGGAGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGCTGTAGACCTGCACATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCACAACTTTGGGCACACTCCCTGTACGCTGTGAAGGAGCACTCAACTCGGCTCTCA
 GCTGAGGAAGCAGCCACTCGCCTTGACCGCTGGACACTAACTACCATGATCTTCCAGCA
 CCTGGAGCAACTCAAGGCATTCTTCGAGAGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCCCAACATAAAGCAACTACTTCCAGTCTCAGCAAGACCCC
 ACCATGGGCAGCCACAAGACGACGCACTGCTGAGTGGCCGCTGGGTGCCAGGCGAGTGTGT
 GAGTGGACAAGCACTGGCACTGGCCCGGATGGAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGCGAGCTCGCGGTGACTGCACTACCCGTTGGCAAGCTGTGTGAGCGAGCTCAGCTGCCAC
 CTTGATGTAGTAACTGCTTGGCTGCACTGGACACTGTGGCACTTACCTTCACTCAGGCTCCCG
 GGACACCAGCTGCATGGTGTGGCGGCTCTGCACTAGGCTGGTGTGTCAGTAGGCTGGCAG
 CAAAGCCTGTGACAGGTCTGTATGGGCTATGGGCTGCACTGAGCTGTGTGGCCATCAGACT
 GAACCTGACATGGCTGTCTGGATCTGAGGATGGAACCTGTGATCATACACACTTACGCGC
 CGGACAGTTTGTAGCGCACTACGCGCTCTGGGTGCCACATTCCTGGACCTATTTTCCACC
 TGGACTTTGGGTCGGAAGCCAGATTGTGGTACAGAGCTCAGCGAGGACGTCGCGGCTTCACTGGCCCT
 CAGGTCACTCATCTCTTGCACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGGCCCT
 GGCAGAGCAGCTCAAGCCCTGACGGTGTACAGAGGACTTGTGTGCTGGGACCGCCGAGCT
 CGCGCCTGCACATCTTCAACTAAACACACTGCTCCCGGCGCGGCTCCCTTGGCCATGAAG
 GTGGCCATCCGACGCTGCTGACCGGTGACCAAGGAGCGACGCTGCTGGTGGCGCTGGAGGA
 TGGCAAGCTCATCGTGGTGTGCGGGGCGAGCCCTCTGAGGTGCGCAGCAGCGAGTTCGCGC
 GGAAGCTGTGGCGGTCTCGCGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATACAAAC
 CTTACTGAGGCGCGCTGAAGTGGCCAGTCCGCGTCTCGGGCGCCGCCGCCGCGGACGGCTG
 CCGCGGAGCGCCCGGCAAGTTCGCGGGGAACACCCGGGCTGGGAGCCAGGGGTTGA
 GCGGGGCCCACTCTGCCAGCTCAGGGATTGCGGGGCGATGTTACCCCTCAGGAGTTGGCG
 GCGGGAAGTCCGCGCCTCGCCGCTGAGGGCGCGCCTGAGGCGCAGCATGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSSGFNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELALET
 MEAAELDEQREKVLVSAECQLVTVVAVVPGLLVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSQEMLRASGLTQKWVQREISNFEYIMQLNTIAGRTYNDL
 SQYPVFPVWLQDYVSPPTLDLSNPAVFRDLSPKIGVVPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGLCLTNEKVGDDVLPWASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSEAAEAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGFWVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCALADTCGIYILISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPFIHLAGSEGQIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRSPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSAVTKERSHVLVGLGEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACACTTGTGAACCTCTCGTGCCCAGGGCTGATGTGCGCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC
 TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTTTGGAGCCCTCATCCTGACCCCTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGTCCGTGCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCC TGGGGGCCATGTGCATCGCCAGCGGCTTCTTCAGCGT
 TTTGCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGGTGGCTCAGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTGTCAGTGAGCCGAGA
 TCGCGCCACTGCACCTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLE
WTLNWWIALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGVGVLSTFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMKSLLKILGKKK
EAPPDNKKRKK

09430203034

FIGURE 26

GAGTCTTGACCGCCGCGGGCTCTTGTTACCTCAGCGCGAGCGCCAGCGCTCCGCGCCCGCT
 GGCT**ATG**TTCTGTTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACCTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACACGACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTTTGACACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGAGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGCACCAACCTCGTCATCTCCAGGGGCCCTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCTGCTCAGCAAAACCTGCTCA
 AGTCTTTGTGTGTTGACAAAGAACCGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCAATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTAGATTGTAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

MFVSDFRKEFYEVVQSRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELATAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDD
LEVPAYEDIFRDEEDEEHSGNDSGSEPEKTRLEEEIVEQTMRRRRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWQDKITQMKYVTDVGVLRH
VSRHNRHNEDEENTLSVDCTRISFEYDLRLVLYQHWLSHDSLNTSYTAARFKLSVHGQKR
LQEF LADMGLPLKQVKQKQFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDLSRSNLDKLYHGLELAKQLRATQQTIASCL
CTNLVVISQGFPLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTGTTCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

094192.08204

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCACTTTTTCATGTGAAC
CACAAGAGGGCAGATACCAGAAAACACCTTCAACCCCAAGGAGATAGACTACGCCCAATTAG
GCTGACTTTTGGCTATAGAAAAGAAAGGAAGCAAGAAAGAGACAGTTTTTTTCGTGAAGCTATA
GCTTCTCCCTTTATTCGAGTCAAGAAACCCCGCTCTCTTGAGCTATTATACAGTTTATCAACT
GAGTAAGATACGCTCCGGTCAAC**ATG**TGCTGACAGCGCCCTGGGTCCCGCTTGGGCAGCGCTC
CTGCTCTTTCTCTCTGATGTGTGATAGTCGTATGTGTGGAGCTACCTTTTGACAGAGCTCTGGC
CAGCGGCTTGCCAAACGGTGTGCTGACTCTGAGGACCCCTGGATCTGCCCATGTATTAACCATC
CCTCTCTCTCCGGCGCCCGCCACCGCCCTGCCTGAGATGCAGACCTTACATTAATTAACCATC
CTGAAGGGTGACAAGAGGGGACCCAGGCCCATATGGGCTGCCAGGGTACATATGACGAGGAGG
TCCCCAAGGGGAGAGCTGGCCCTCAGGCGAGCAAGGGTGACAGAGGGGAGATATGACGAGCCCG
GGCCCGCTGTCCAGGAAGCGCTTCTTGCTCTCTCAGTGGGCCGAGTATGAGGCCCTGCACAG
GGCAGGAGCTTCCAGACGCTGCTCTTCGAAGGGTCTTTTGAATCTTGATGGGTGCTTTGA
CATGGCGACCGGCGAGTTTGCTGTCTCCCTGCTGGCATCTTGAATCTTGACGCTCAATGTGC
ACAGTCTGGAATTACAAGAGAGCTACGTGCACATATGATACACAGGAAGAGGCTGTATCT
CTGTACGCGAGCCCGCAGCGACGCGACGATCATGCAGAGCGAGTGTGATCTGGACCTGG
CTACGGGACCGCGCTTGGGTGGCGCTCTTCAAGCGCCAGCGAGAACGCCCATACAGCA
ACGACTCTGCACACCTACATCACTTACAGCGGCCCTCACTCATCAAGCGCGAGGACAG**TCG**AGG
CCTCTGGGCGACCCCTCCCGCTGGAGAGCTCAGGTGTGGTCTGCTCCGTCCGTGCAGGGCTCAG
TTTGCACTGCTGTGAAGCAGGAAGGCGGAGGAGGTCCCGCGGACCTTGGCATCTCTGGGGA
CCTTGCTCTATCTTGCTGGCTGCCATCATCTCCCTCCCACTCTCTCTGCTCTCTCTCTCT
TGGACCTATTTTAAAGAGCTTGTGAACATAAATCCCGGGTTCGATGTAATGCAGATTCT
AGCATCTCTCAAACTTGGAAATGCATTCGGAATACCCGGGTTCGTTTAAATGCAGATTCT
GACTCAGCAGGTTCTGAGTGGGTCTAGGATTTCTGTTTCTCATATGTTCTGGGTGATGCTG
ATGGGTCAGTCTATGAACCACTATGAGGCGAACAGGTTTACGAGTTCTCAATATCTAG
TACTTTTCGACAATTCTTGAATTTCTCCCGACATCTAGAAATCTCCCAACTATTTTCTCTG
TAAGCTCAGAGCTCTTGTCTTCAAGCATTTCTTCTGCCCTAGGTCCTCATGTGGCTGGGATTAC
ATGGCGCTCTACCATGCTTGGCTAATTTTGTATTTTATAGAGATGGGTTTACCATTA
TGGCTGGGCTGGTCTTGAATCTCTGACTCAGTGAACCCCGCTCGGCTCTCAAAAT
GCTGGGATTAGAGTGTGAGCCAGCTGCTCGGCAATTCAAACTTTTAATTTCTCTCAT
CCCCCTGGGGCTCCCCCTGATATGTTCTCTTTACCCCTTCCCCCTCTCTCTGTCTCAGGCC
TGACCACTCAGCCACCGTCTCAATTTATTCATTAACATTAACACTGAGCATCTCTGTGCT
GGGTCCCGGGAAGGTTGAGGGGTGACAGAGCCGCTGCCCTGCCCTCAGTGCATGGCCCA
CTCCAGCCAGGCGGGGAGAGATGTGTACATAGTGTTTAAAGCAGACCCAGGCTCATGGG
GCCCTGTGTTCTGGGTGTTCAAGTGTCTGCTGGTCTCTCAATTACCCACTGCTCCCCAAGGCTGG
TGGACGGGGTCCCGTGGCAGGGGCGAGTATCTCTTCCCGTTCTCATCCACTCTGCCAG
TGCTCATCTGTACAGCAAAACCCAGGGGGCTTGCCAGGCTCAAGGTTCTGTGAGGAGGAG
ACCCAGGAGTCTTGGGGCATTTGGGGGGTGAAGTGGCCCCGGAAGATGGAACCAACACCCA
TAGCTCTCCCCACAGCTTACAGCCATCTTCCGAGAAGACTGCCCTCTCCACTGGGATCCC
CTTCTCGCTCTCTCCAGGGCTTCTGCCAGGCTTGCTCAGTCCCTTCCACCAAGATCATCT
GAACTTCCGTTTCCCCAGGGCTCTCAGCTGCGCTCAGACACTGATGTCTGTCCGCCAGGTGCT
CTCTGCCCTCATGCCCTCTCACGGCCGAGTGGCCCGACTCTCAGGGTTTATCAAGTGT
CTAAGGCCCCGGGTGGGCACTCTCTGCTCTCAGAGCCCTCTCTCGGCTTGGTGTGCTTTTAC
AAACACCTTCAGGAGAAGGGCCAGGAAGCCCGAGGCTTTAGAGCTCTCAGCAGGTTCTGGGG
AGCTAGAGACAAGGAGGACCTCTAGCCCTTCCGTTCTCTTCCAGGGTGGGTTGGCTGGT
GTTCCTCTAGCTCTTCAAACCCAGGATGGCCTGGCCTCTCCCCAGAGGAGGAGCGCTCGCG
CCATTTGGTGTCTCATGACACTCTGGGGCTGAGGTGCGCCCGGGGGTGATCTTGTTGCTCAC
AGCCGAGGGAGCGCTGGCTCATGTGGCCAGATGACGGAACAGGCTGTGACCAAGTGCAGGA
AGACTGTGTCTATAAACACCTCTGCTGATCTCGGCTGCTGTGACCCCGCCAGCGCTGCC
GTCCAGCATGATTAAAGATGCTGCTCTCTCTTGCAAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPPGQSGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

C1q domain proteins.

amino acids 144-178, 78-111 and 84-117

094199-73304
T0222-26460

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCACCCGCCAGGAAAGACTG
 AGGCCGCGGCTGCCCGCGCCGGCTCCCTGCGCCGCCCGCGCTCCCGGGACAGAAG**ATG**TG
 CTCAGGGTCCCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCGAGGAGCTTTGCCGGCCTGCCGGGCTGACAGCTCCTGGACCTGTCAC
 AGAACAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCGGCGCCT
 CGAGCGCTCTACCTGGGCAAGAACGCATCCGCCACATCCAGCCTGGTGCTTCGACACGC
 TCGACCGCCTCTGGAGCTCAAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGTGGC
 CTGCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGAT
 CTTGGACACTGCCAACCTGGAGCGCTGCGGCTGGCTGCTGGGGCTGCAGACGTGGACG
 AGGGGCTCTTACCGCCTTGGCGAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCGCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAAGAGCTGGATG
 TGAGCAACCTAAGCCTGCGAGGCCTGCTGCGGACCTCTCGGGCCTCTCCCCCGCCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTGTGGCCCTG
 GGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTGGCTGCCAGCCACCACC
 ACCACAGCCAGCTGCCACACGAGGCGCTGGTGGCGGAGCCCAAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCA
 CTGCCCCACCGACTTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACCAGGTCCTTGACCTGGCCTCGAGCCGTTGAGCCGCTGAGCCCGCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACAGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCCTTTGGGG
 CCGGGCGGGTGCCGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGTCCA
 CTCCAACACGCCCCAGTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTATTGCGCCCG
 CCCTGCGCGCGGTGCTCCTGGCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG
 GGGCGGGCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTTGGGGCCAGGGGCTGGGCCCT
 GGAAGTGAGGGAGTGAAGTCCCCTTGGAGCCAGGCCAAGAGCAACAGAGGCGGTGGAG
 AGGCCCTGCCAGCGGCTGTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTC
 CAGTCACCCCTCCACGCAAGCCCTACATCT**TAAG**CCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACACAGTAAAGTTCTCAGTCC
 CAACCTCGGGATGTGTGACAGACAGGCTGTGTGACCACAGCTGGGCCTGTTCCTCTGGA
 CCTGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGACGTCCCTGGGACGGCG
 GGCCTGCCATGTGCTGGTAACGATGCTGGGTCTGCTGGGCTCTCCACTCAGGCGTG
 CCCTTGGGGCCAGTGAAGGAAGCTCCCGGAAAGACAGAGGAGAGCGGGTAGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTCAAACTCAGAGCAAGGACTTTGGTTTTTGTGAAGACAAACGATGATATG
 AAGGCTTTTGTGAAGAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P
G I L D T A N V E A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S
S S L A P T W L S P T A P A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E
G F T G L Y C E S Q M G Q G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A
V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G
P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

FIGURE 33

GAATCATCCACGCCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAAATAAGTGGTAAAAATCCTTGGAAAATCAATGAGAGCTCATCAG
 AAACATTTTACATATTTTGTAGTATTTGTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAAACATGTCTCTAAGAAAGGCTTCCCGAGAGCTTG
 ACCCCAGCCACCAACAGCACTGGATTTATCCTATAACCTCCITTTTCACTCCAGAGTTCAGA
 TTTTCATTCTGCTCTCCAACTGAGAGGTTTGTATCTTATGCCATAACAGAAATTCACAGCTGG
 ATCTCAAACCTTTGAAATCAGCAAGGAGTTAAGATTTAGATTGTCTTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGCTCAGGATTTTGTATCTTTCTTTTAACTGACTT
 TGACACCATGCTATCTGTGAGGAGGCTGGCAACATGTACACCTGGAAAATCCAGTTTGA
 GTGGGGCAAAAATAGCAAAAATCAGATTTCCAGAAAATGCTCATCTGCATCTAAATCTGTC
 TTCTTAGGATTCAGAACCTCTTCTCATTATGAAGAGGTAGCCTGCCATCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATCGACACAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAAATTTGTAAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTCTTCTTACAATTTGTTTGGCATACATCATGAGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGACTAC
 TCAAAATCTGATTAATGAGAATCATAAAAATGGAGCATGTACATTTTCAAGTGTTTTACATTC
 ACAGGATAAAATCTATTGCTTTTGGCAAAAATGGACATAGAAAACCTGACAATATCAAAATG
 CACAAAATGCCACACATGCTTTTCCCGAATTTATCCTACGAAATTTCAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACAGTGTGTTTAAAGAACTATCCAATCGCTCACTTGAAGAACTCT
 CATTTTGAATGGCAATAAAGCTGGAGACACTTCTTTAGTAAGTTGCTTTGGTAAACACACAC
 CTTTGGAAAGCTTGGATGTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTACATAAATAAATTTGCTGTCTGCTTCAG
 GTGCTTGGCCAAAAGTATTTCAATACTTGACCTAAATAATAACCAAAATCCAACCTGTACCTA
 AAGAGACTATTCATCTGATCGAGTCCCTTACGAGAGACTAAATATTGCATTTAAATTTTCTAAGT
 CTCCCTGGATGCACTGATTTTCACTAGACTTTTCACTGATGAACTTGAATGAACTTCACTT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAA
 ATCCATTCGGGTGACTCTGGAATTAATAAAATTTTCACTCAGCTTGAACATATTGAGAGGTC
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCCCTTAAACCTAAGGGGAAGTAG
 GTTAAAGACGCTTCACTCCACGAATTTATCTTGCAACACAGGCTCTGTGATTGTCAACCTATG
 TGGTTATTATGCTAGTTTCTGGGTTGGCTGTGGCCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGAGTGCTAGGTCATGCAACACAAACATGGCACAGGGTTAGGAAAACAAACCCA
 AGAACAACCTCAGAGAAATGTCCGATTCACGCAATTTATTCATACAGATGAAATGATTTCTC
 TGTGGGTGAAGATGAATTTGATCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGTATTGCT
 CTTTATGAAGACTTCTTTGCCCAACCAATCTCTCCATGAAAATTTGATCATATAAATCTTTATC
 TTACTGGAACCCATTCATCTTATGCTATCCACAGGTATCATAACTGAAAGCTCTCCT
 GGAAAAAAGAGCATCTGGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGC
 ACCCTCGAGCTGCTATTAAATGTTAATGTATTAGCCACAGAGAAATGTATGAATCGCAGACA
 TTTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTGTCT
ATAAAATCCCAAGCTCTTGGGAAGTTGGGGACCACATACACTGTGGGATGTACATTTGATA
CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAAATGGTTATTCCCTCATATA
TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACACCTTCACAAGTTTATAAGG
GCTTATGGAATAAAGGTTTCAATCCAGGATTTTATAATCATGAAAATGTGGCAAGTGTG
AGTGGCTCACTCTTGAATCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACAGGTC
CAGATGGAGCACTCTGGCCAAACATGGTGAACCCGTCTCTACATAAAATACAAAAATTA
GCTGGGCGGATGGTGCACGGCTGTAGTCCAGCTACTTGGGAGGCTGAGGAGGAGAATCG
CTTGAAACCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCACTGCATCCAGCCCTGGT
GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGGAAAAATCC
TCATGGCCACAAAATAAGGTTCAATTTCAATAAATATAGTACATTAATGTAATATAATATA
CATGCCACTAAAAAGAAATAAGGTAGCTGTATTTTCTGGTATGGAAAAACATATAATAT
GTTATAAATATTAGGTTGGTGCAAAACTAATTTGTGGTTTTTGGCAATGGAATGGCAATGAA
ATAAAGTGTAAAGAAATCTATACAGATGTAGTAACAGTGGTTTTGGTCTGGGAGGTTGGA
TTACAGGGAGCAATTTGATTTCTATGTTGTGATTTCTATAATGTTGAATTTTGAATTTGA
ATCTGTATTTCTTTTATAAGTAGAAAAAAATTAAGATAGTTTTTACAGCCT

004455-032601

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPMICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTCKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFRKTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENCSPWETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNNIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMVLGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

09041999:000001

FIGURE 35

GGGGGCTTTCTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAAGGACCGGCCCTCGGAGGGGTTCGGGGGAAAGG
 GAGGGAAGAAAGGAGGGCGGGGCCGGCCCCCTCGCCCGCCGCGCCGCTCTCGCGGCCCTGTCTCGCCCGCCGGC
 CGAGCCAGCCAGCCGCGCCGCGCGCGCTCACACGCGCAGCAGCGCGCGCCGCTCCCGCGCCCAAGAGCGCGCGCT
 CTGCTGTGGCTTGCGCCCTTGGCCCGGCCAGCTTCTGCGCCCGCAGCCGCGCCGCGCGCCCGCGCTGACCTGTGA
 CCTCGCCTGGGGCGGGGCGGAGGAGGCTATGCTCCCGCCCGGGGACCGCTACCCAGGCTGGCCCTGTGCTC
 CTGGCAGTGACCTTGGCGGGGTTCGAGGCCAGGGCGAGCCCTCGAGGACCTTGATTTATTCAGGCGAGGAT
 CTGGAGCGGGAGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCCGCCCTGCCTCGGGGGC
 CCGGGGAGGAGTGGGAGCGCGCGCCCGCAGGAGCCAGGCGCCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC
 AAGAGGGAGAAAGTCTGGCTCCGGAGCGCCCTCCACCAGGTAAACACAGCAACAAAAAGTTTATGAGAACCAGAG
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGCTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAAATGATTTTTATGACGGAGCGTGGTGCGGGGGAAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGCGCCCTGACCAGATTCACTGGTCTCATCACTCAAGGGA
 GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAAGCAATGACAGCCACAGCTGGGTC
 ACTGTTAAGAAATGGATCTGGAGACATGATATTGAGGGAAAAAGTGAAGAGGAGATCCCTGTCTCAATGAGCT
 ACCCGTCCCATGGTGGCCCGCTACATCCGATAAACCTCAGTCTGGTTTGATAATGGAGAGCATCTGCATGA
 GAATGGAGATCCTGGCTGCCCATGCCAGTCCATTAATATTATCACCGCCGGAACGAGATGACCACTCAT
 GATGACCTGGATTTTAAGCACCAATATAAGGAAATGCGCCAGTGTGATAAGATTGTGAATGAAATGTGTTC
 CAATATCACAGAAATTTACACAACTTGGAAAAAGCCACAGGGGCTGAAGCTGTATGCTGTGGAGATCTCAGATG
 ACCCTGGGGGACATGAAGTCTGGTGAAGCCGAGTTCACACTACATCGCGGGGCCACGGCAATGAGGTGCTGGGC
 CGGGAGTCTGCTGCTGCTGGTGCAGTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATGCTCCACCT
 GGTGGAGGACGCGGGATTACAGCTTCTCCCTCCCTCAACCCGATGGCTACGAGAGGCCATGAAAGGGGCT
 CGAGAGCTGGAGGCTGGTCCCTGGGACGCTGGAGCCACAGATGGAATTGACATCAACAACACTTCTCTGATTATA
 AACACGCTGCTCTGGGAGCAGAGGATCGACAGAAATGTCCGAGGAAAGTCCCAATCACTATTTGCAATCCC
 TGAGTGGTTTCTCTCGGAAATGCCACGCTGGCTCGCGAGACCAGAGCAGTCAATGCCCTGGATGGAAAAAATCC
 CTTTTGCTGCTGCGCGCAACTCTGAGGCGCGGAGCTGTGGTGGCGTATCCCTAGCAGCTGGTGGCGGTCGCC
 TGAAGAGCGCAGGAACACACCCCCACCCCGATGACCACTGTTCCGCTGGCTGGCCTACTCCCTATGCTCCAC
 ACACCGCCTCATGACAGACGCCCCGAGGAGGCTGTGCCACAGGAGACTTCCGAAGAGGAGGAGGCACTGCA
 ATGGGCGCTCTGGCACACCGTCTGCTGGAAGTCTGAACGATTTCACTTACTCATCAAACTGCTTCAAGATG
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGATAAACCGGAATC
 TCTGATCGTGTTCATGGAGCAGGTTTATCGTGGCATTAAGGCTTGTGAGAGATTTACATGGAAGAAGATCC
 CAAAGCCCATTTATCTCCGTAGAAGGCATTAACCATGACATCGGAACAGCCAGATGGGAGTTACTGGCGCTC
 CTGAACCTCGGAGATATGTGGTCACAGCAAAGGCCGAAAGTTTCACTGCATCCGCAAGACTGTATGGTGG
 CTATGACATGGGGGCCACAGGCTGTGACTTCACATTTAGCAAAACCAACATGCCAGGATCCGAGACATCTMG
 AGAAGTTTGGGAAGAGCCCGCTCAGCTGCCAGCCAGGCGCTGAAGCTCGGGGGCGGAAGAGACGACATAGT
 GGGTGAACCTCTGGGCCCTTGAGACTCTGTGGGACCCATGCAAAATTAACCAACCTGGTAGCTCCATG
 TGACTCACTCAGCTGTTGTTTTCCTCTGAATTCAGAAGTGCTGGAAGAGAGGGTGCATTGTGAGGCGAGGTCC
 CAAAGGGGAAGGCTGAGAGCTGAGGCTGTTTCTTTCTTTGTTGCCATTTATCCAAATTAATCTGGACAGGCA
 GCAGAGAAAGCTGATGGGAGTGAAGAACTCAGCAAGCCAACTGGGAATCAGAGAGAGAGGAGAGAGGAG
 GAGCCTGTGCGTTACAGACCTCTGGCTCATAGAAAAGGATTTGCTGCTTCCCTCTTTGCTGTGGACGACCG
 GTTCCACGTGCAATTTGCAATTTGACAGCTAAAAATTCAGCAGTTTCCAGCTGGGCTGTCCCAATGTTACAA
 TTTGAGATGCTCCAGGCGCTCTAAGAGATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATTA
 ATTCTGTGTTCTTTGACAAATAGCGCTATTGCCAAGTCACATCAGTGAGCCTCTGGAATCTGTTAGTCTCT
 TTTTCAACAAAGGAGTGTGTTCAAGAAAGGAGAGAGGCTGAGATCTCTCAGGAGATTGTTGGGCGCAGCA
 TGGAGCTTCTTGTGCAAAATTTCTGGGTCCATAAACACACCCCAAGTCCCTGCTGATCCAGTCCCGCTGGAGTT
 CCCCAGTTAGGAGAGCCAGAGGTGCCAGCTTCTGAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC
 CTGCTAGGATGGAAGAGCCAGAAAGTGGGTGGCTCAGGCCCTCTCTGCTGTAGGATTTGCCCTGTGTG
 GAATTGAGTGTCTATGGGTTGGCCTCATATCAGCTTGGAGTATTTTGATATTTAGAATGCCAGATCTTCA
 GATTAGGCTAAATGTAATGAAACCTCTTAGGATTATCTGTGAGCATCAATTTGGGAAGAAATTTGAATT
 CTTGCAAGAAAAAGTATGCTCTCACTTTTGTAAATGTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAAGCAAAATGTTAGACCTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEFELETFSPPPLP
AGPGEWEWRRPQEP RPPK RATKPKKAPKREKSAP EPPPGKHSNKKVMRTKSSEKAANDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGI DINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKEGFASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRG

[illegible]

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSSRGSSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPQHFNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGGTAVYNNNMVYNNMYNTGNIARVNLTTNTIAVTQTLPNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVLYATRTMNTRETEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

0941992.08293

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTTGTGACGTTTGTGGAGATGGGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTTGTGTGGAAAGTGGCCCGTGTGTGCTATGCCGATGCTGCCTAGTGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCTTTGGAGTATGTTAGCTTTG
 TGTAAATGTTGATACCGAGTATGGAAGAACACTGAATAAGATTCTTGCATTTTGTGAGAAATG
 AGAAAGGTGTTGTCTGCTTGAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTTCTCTTTTACTAATGATCAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTTGGGGCATTTCTTATCCAGAAGGAACCTTTTACAACCTGTCTGGTTTATGTAGGCATG
 GCAGGTGCTCTTTGTTTTCATCCTCATACAACCTAGTCTTACTTTATGTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAGAGAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCGAATTTATCTGCTGTCTTTAGTTGCTATGCTCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTCAGAAAAACAGGCGGTTTACAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACCTGCCAAAAATCCAGATCAACAACCAAGATCTGGTT
 TGTACAGTCTTCAGTAATTTACAGTCTACACAATGTATTTGACATGGTCAGCTATGAACCAAT
 GAACCAAGAAACAAATTTGCAACCCCAAGTCTACTAAGCATTAATTTGGCTACAATAACAACGAC
 TGTCCCAAGGAAGGAGGAGTCAAGTCAAGTGGTGGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTTGTGATTTTATTTCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA
 CTGAGTCTAACAGTGTATGAATCTACATTAATAGAAGATGTTGGAGCTAGAAGTAGGATGATC
 ACTGGAGGATGGGGACATGTTTCAAGGAGCTAGATAATGAAGGGATGGTGTCACTTACA
 GTTATTCTCTTCTTTCACCTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACGTGGTCCAGGTATGAACCCCTCTGAGATGAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTCTCAGTTGGATTTGGCATCGTCTGTATGTTTGGACACTCTGGGACCCTTTGTT
 TTACAATTCGTGATTTTGACCTGAAGTGTAGACTTCTAGCATGAAGCTCCCATTTGATTTATGC
 TTATTTGAAAAACAGTATTTCCCACTTTTGTAAAGTTGTGTATGTTTGTCTTCCATGTAAAC
 TTTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTGTCAATTTTGTATTTTCTTACCAA
 GTGCATTGATATGTTGAAGTAGAATGAATTTGCAGAGGAAAGTTTATGAATATGGTGAAGT
 TAGTAAAAGTGGCCATTATTTGGGCTTATTTCTGTCTATAGTTGTGAATGAAGAGTAAAA
 ACAAAATTTGTTTGAATTTTAAAAATATATAGACCTTAAGCTGTTTACGAAGCATTTAA
 GCAAAATGATAGCTGCTTTTTTAAAAATTTTGAATATTTGATGTGTGCTGGCAGGATGACTGCAAGAAC
 ATGGTTTATTTTAAATTTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTACCTTGTGAAGTAAATTTACACAGTAGGAGGAGTGTGTAGTGGACAATAGTGTAGG
 TTATGGATTGGAGGTGTGCTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCTTTTCCGACAGTGTGCTGAACCTGTTTGGTTGTTTAAACTCATGAAGTATGGGTTTCA
 GGAATGTTTGAACCTCGAAGGATTTAGACAAGGTTTTGAAGAGGAATATCATCTGGGTTAGA
 AGGAAGTGTTTTGAAGTCACTTTGAAGTTAGTTTTGGGCCAGCAGCGGTAGCTCACCTTT
 GGTAAATCCAGGCTTTGGGAGCTTAAAGTGGGTAGATTACTTGGCCCGAGGAATTCAGACCA
 GCTTTGGCACATGGTGAACCTGTTCTATAAAAAATACTGGCTTTGAGCATATGCTCTGGTGT
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCGAGGCCAAAGGTTGCAGTGGAGCAAGTCA
 CGTCACTGCACCTTACGTGGCACAAGTAAAGCCAAAAAATATATATATTAATGAATCAAGG
 AGGCCAAATTTTACAGGGAGGAAGTAACTGCCAAACCCATGAGCTTTAGTAGGTACTTAT
 ATAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAATACAGACTATAATA
 TCTCAGATAGCTAATTAGAAATTTCAAGTTGGCCAATAATAGCAATCTCTCTGACATTTAA
 AATATGATTTCTATTCAAATCATGCAATTTGATTTACACCTCATACTGTGATATTAATGT
 GATGTGATTTGCTGGTGTGCTGAGCATGACCCATAAACAGGTCAAGAAGATGATGGAAATGTTT
 AGAATAAACTCTGCTTTATAGTATACTACACAGTTCAAAGAGTGTAAAAATGCTTTTGTAT
 TTACTGGCATGTGAATGAATATATAGATTATTTGTAACCTTTCAACCTGAAAATCAAGCAGT
 ATGAGAGTTTAGTTATTTGTATGTGTACTAGTGTCTAATGAAGCTTTTAAATCTCAAAAT
 TCTTCTTTAAAAATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATTTCCCAACC
 TTATCTGTGTGTAGACATTTGATTTCCACAAATTTTGAATGGCTGTGTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

100220.26614662
 20240404.100220.26614662

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMylTWSAMTNEPETNCNPSSLISIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAGTATGATCTA
TGCACTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

094199.082801

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACITTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

094459-00000
00000-00000

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAACAACCTCCACTGTAACCTAGATTGATCTATGCACTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

094192.02501

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGCGCGGCCCTCTCCAAT
 GGCAAAATGTGTGTGGCTGGAGGGGAGCGCGAGGCTTTCGGCAAAGGCAGTCGAGTGTTCGACAGCGGGGGGACG
 TCCTCTGAAAGCAGATTAAGAAAGAAATTTATTACGTGTCTTACGAGGGAGCGCCCGCGCGGGCTGTGCGC
 ACTCCCCGCGGAACATTTGGCTCCCTCAGCTCCGAGAGAGGAGAAGAAAGCGGAAAGAGGCGAGATTCC
 GTGCTTTCAGCCCAAGTGGACCTGTGATGGCCCTCTGAATTTATCAGTATTTGATTATTATAGCGATTGAC
 CCTGTGGTTTGTGTGTTACGCACACACAGCTGCACACAAGGCTCTGGCTCCGCTCCCTCCCTCGTTTCAGCTG
 TGGGCGAATCCCACATCTGTTTCTCACTCTCCCGCAGGGCGCAGGAGCGAGATGTGTGCGAATCTGCGAGTG
 AAGAGGGACGAGGAAAAGAAACAAAGCCACAGACGCACTTGAGACTCCCGCATCCAAAGAAAGCCAGGAT
 CAGCAAAAAAAGAAAGATGGGGCCCCCGGAGCTCTGTGTGTGCTTGTGTCCCAACTGTGTTCTCCCTCTGGG
 TGGAAAGCTCGGCCCTTCTGTGCGCACACCGCTTGAAGGCAGGTTTCAGAGGACCGCAGGAACTCCGCCCA
 ACATCATCTGTGCTGTGACGGAGCAGCAGGATGTGGAGTGGGTTCCATCGAGTGTGATGACCAAGACCCCGGCG
 ATCATGGAGCAGGGCGGGGCGCATCTCATCAACGCTTCTGTGACCACACCCATGTGCTGCCCTCACGCTCCTC
 CATCTCTCACTGGCAAGTACGTCCACAACACACACCTACACCAACAATGAGAATGTCTCTCGCCCTCTGG
 AGGCACAGCAGAGCGCGCACCTTTGCCGTGTACTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACAACGGCTCTACGTGCCACCGGCTTGGAGGAGTGGGTGCGGACTCTTAAAACTCCCG
 CTTTTATACTACAGCTGTGTGCGAACGGGTGAAGAGAAAGCACGGCTCCGACTATCCCAAGGATTACCTCA
 CAGGACTCATCAACCATGACAGCGCTGAGCTCTTCCGACGCTCCAAGAGATGATCCCGCCAGCGGCCGCTCTC
 ATGGTCATCAGGCATGCAGCCCCCAGCGCCCTGAGGATTCAGCCCCAATATTACGCTCTTCTCCAAAGC
 ATCTCAGCAGCATCAGCCGAGCTACAACACTACGCGCCCAACCCGGACAACACTGGATCATGCGGTACAGCGGGC
 CCATAGAGCCCATTCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTCGACAGCCCTCATGCTCGGTGAC
 GACTCCATGGAGACGATTACAACATGCTGGTTGAGACGGGGGAGCTGGACAACACGTACATCGTATACACCGC
 GCACACGAGATTCACATCGCGCAATTTGGCTGGTGAAGGAAATCCATGCCATTTAGGTTTGATCATCAGGG
 TCCGCTCTCATGTTGGAGGCCCAACGTGGAGCGGCTGTCTGAATCCCCATCGTCCCTCAACATTTGACCTG
 GCCCCACCTATCTGGACATTCGAGGCTTGGACATACCTCGGATATGGAGCGGAATCCATCTCAAGCTGCT
 GGACACGGAGCGCGCGTGAATCGGTTTCACTTGAAGAAAGAGATGAGGCTCTGGCGGGACTCTCTCTGTGTG
 AGAGAGGCAAGCTGTACACAAGAGAGACAAATGCAAGGTGGACGCCAGGAGGAACCTTTCTGCCCAAGTAC
 CAGCGTGTGAAGGACCTGTGTGAGCGTGTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAATGGCAGTG
 TCTGGAGGACCGCCAGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATCGGCTGGCGGGCAGCAGAGGCC
 TCTCCAAGCTCTGCGCCAAAGTACTACGGGCGAGGCGAGCGAGGCTGCACCTGTGACAGCGGGACTACAAGCTC
 AGCTTCCGCGCAGCGCGGAAAATCTTCAAGAAAGATACAAGGCCAGCTATGTCCGAGTCTGCTCCATCCG
 CTCACTGTGCCATCGAGGTGGACGGCAGGCTTACCAGTATGGCCTGGGTGATCGCGCCAGCCCGGAACTCA
 CCAAGCGCGCATGBCACAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTCTAGTGGCACTGGAGG
 CTTCCGACTACTCAGCGCCCAACCCATTAAAGTGACACATCGTGTCTACATCTAGAGAACGACACAGTCCA
 GTGTGACCTGACTCTACAGTCCCTCAGGCTTGAAGACCAACAGCTGCACATCGACACAGAGATTGA
 CCTCTGCAGCAAAATTAAGAACCTCAGGGAAGTCCGAGTCACTGAAGAAAGCGGCCAGAGAAATGTGAC
 TGTCAACAAATCAGCTACCAACACAGCAGCACAAGGCGCCTCAGCACAGAGCTCCAGTCTGATCCTTTGAG
 GAAGGGCTCGAAGGAAGAGGACAGGTTGGCTGTCGCGGAGCAGAAGCGCAAGAAAGAACTCCGACAGCTG
 TCAAGCGCTCGAGAACACAGCAGCTGCAGCCTCAGGCTCACGTGCTTCCACCAGCAGACAGCAGCTGG
 CAGACGGCGCTTTCTGGACACTGGGGCTTTCTGTGCTGCACCGCGCCAAATACACGTAAGTGTGTGAT
 GAGGACCATCAATGAGACTCAATATCTCTTCTGTGAATTTGCAACTGGCTTCTAGATACTTTGATCTCA
 ACACAGGCCCTCAGAGCTACAGTATGATGAATCAGTGAACACACTGGACAGGGATGTCTTCAACAGCTACAGTACAG
 CTGATGGAGCTGGAGGCTGCAAGGGTTACAGGAGTGTAAACCCCGGACTCGAAACATGGACCTGATGAGG
 AAGCTATGAGCAATACAGGCAGTTTCAAGCTCGAAGTGGCCAGAAATGAAGAGACCTTTTCCAAATCACTGG
 GACAACCTGTGGGAGGCTGGGAAGGTTAAAGAAACACAGAGGTGGACCTCAAAAACATAGAGGCCTCACTCTG
 CTACACAGGCATGAAAAACATGTGGTGATTTCAGCAGACCTGTGCTATTCAGCGAGGCTCGAGAGCTGAGAAGC
 AAGCAAGCACTCTCAGTCAACATGACAGATTTGAGAGGATAACACAGGAGGACAGAGATTAATTCAGGAAGTCC
 ATCTTTGGCCCTGCTTTGCTTTGGATTATACCTACCACTGCACAAAATGCAATTTTTCGATCAAAAAGTCT
 ACCACTAACCTCTCCCCAGAAGCTCAAAAGGAAAAAGGAGAGAGGAGGAGAGAGATTTCTTGAAATTTCT
 TCCCAAGGGCGAAGTCAATTTGAATTTTAAATCATAGGGGAAAAGCAGTCTGTTCTAAATCTTATTCTT
 TTGGTTTGTCAAAAGAAAGGAACTAAGAGCAGGACAGAGGCAACGTGGAGAGCTGAAAACAGTGCAGAGAGG
 TTTGACAAATGAGTCAGTACGACAAAAGAGATGACATTTACCTAGCACTTAAGACCTGGTGGCTCTGAGAGAAA
 CTGCGCTTCATTTGATATATGTGACTATTTACATGTAATCAACATGGGAATTTTAGGGGAACCTAATAAGAAAT
 CCCAATTTTCAGGAGTGGTGTGCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAA

MGPPSLVLCLLSATVFSLLGGSSAFLSHRLKGRFQRDRNRIRPNIIVLVDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFGKYLNEYNGSYVPPGKWEVGLLNSRFYNTLCRNGVKEKHGSD
YSKDYLTLTINDSVSFRTSKKMPHRPVLVISHAAPHGEDSAFQYSRLFNPASQHITP
SYNYAFNPDKHWMRYTGPMPKPIHMEFTNMLQKRKLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEYFDIRVPFVVRGPNVEAGCLNPHIVLNIIDLAPTILDI
AGLDTPADMDGKSLILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNKDVAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKGLKHCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYIENDTVQCDLRLYS
LQAWKDHKLHIDHETLQNKIKLLREVRHGLKKRKEPEECDCHKI SYHTQHKRGLKHRRGSSL
PEFRKGLQKHDVWLRLREQKRKKLRLKRLKRLQNDNCTSMPLGTCFTHDNQHWQTAPFWTLG
HFCACTSANNNTYKMPRTINETHNFLFCEFATGFLEYFDLNTDYPQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRKRKWPMPKRPSSKSLGQLEWEGWEG

0000000000

00000000

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQCDVERNRTAAGGNRVRR AQWPFR
RRGHLGI FHHHRHPGHVSHV PNVGLHHHHHP RHTPFHHLHHHHHP RHHHPRHAR

108280.2661460

GGCGGCTGCTGAGCTGCCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTGGACCTGCTA
CTACTGGGCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCTGAGTGAAGGTGAGGAATCGCCCTCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCTTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCTCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAATGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGCTAACCC
ATGGCCTGCACCCCTCTCGAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGTTGGGGAGGAGGGGTTCTGAGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCTCACTGCCTTTAGGCTCCGAGGCCAGAGGAGCCA
GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTGTTGTCTTTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTGTTACCTGGAACAAAA
AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDYFVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

12320.26460

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCTTGGTGCCCGGCTCCCT
 GCCCCGCGCCAGTC**ATG**ACCCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCACCACATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

094199-00001

FIGURE 54

CCCGGGAACGTGTTCCCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
 CCCGCGCCAGTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
 TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
 CTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
 CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
 CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
 CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
 AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
 TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
 ATGGCCATGGTGCCACCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
 CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
 AATAATAAATTTAAAAAECTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAACTTAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGGGCGGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATTGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACCAAAAATCTATTTGTGGTATGCACCTTGATTAACCT
 ATAAAAATGTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTAATAATAAAAGAAATTACAAAAGAAATATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCAATGAAAGTGTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAATTCCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGCTCCCAAGGGGTGAGTGGACGTGTGGAAGAGAGAAGCACCAT
 GGTCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCAT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVI
ATTIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

094392-03204
10220-263490

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTTGAATGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

J03250.2361650

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTTCAGAAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

0941992.00001

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

J03250.261460

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCGTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

094322-082801
T02280.266460

FIGURE 62

GGGAGGCTGTGNC CGTTTTTGT TTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTA CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTGCGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

CGGAGGCTGTGNC

FIGURE 63

CGACGCCGGCGTG**ATG**TGGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGCTCC
 TCTGCAAAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCCTTTCTCCGAAGATGTC
 AAACGGCCCCCAGCGCCCTCGTTAACTGACAAGGAGGCCAGGAAGAGTTCTCAAAACAAGC
 TTTTTACGCCAACCAAGTGGCGGAGAAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
 GCCTGGCTGCAGCTGCAATTTAGCTTAAAGCTGGCAAGCGAGTCTGGTGTCTGGAAACAACAT
 ACCAAGGCAGGGGGCTGCTGTCTACCTTTTGGAAAGAATGGCTGTGAATTTGACACAGATCACTG
 CCATTACATTTGGGCGTATGGAAGAGGGCAGCAGTATGGCCGTTTATATCTGGAGCCAGATCACTG
 AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC
 AATGGCGGAAAGGAGTACCCCATGTACAGTGGAGAGAAGCCCTACATTCAGGGCTCAAGGA
 AAGTTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGTTTAAAGTGGTATCCA
 GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCCGTGGTTTCAGCTCCTCGAC
 AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCCAGACTTCCCTGA
 GGTCTCGACAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTAGACTTCCCTGA
 CTTACGGTGTCAACCCCAACCAAGTCGCTTTTCCATGCAAGCCCTCTGGTCAACCACTAC
 ATGAAAGGAGGCTTTTATCCCCGAGGGGGTTCCAGTGAATTTGCCCTTCCACACCATCCCTGT
 GATTACGGGGCTGGGGGGCTGTCTTCAAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
 CAGCTGGGAAGGCCGTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
 CCGATCCAGTGGTCTCAACACAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
 CCGCTGCCCTGCCAGTGTGAAGCAGCAACTGGGGACGGTGGCGCCCGCTTAGGCATGACCT
 CTGTTTTCATCTGCCGCGAGGCACCAAGGAAGACTGCATCTGGCCTTCCACCACTACATAT
 GTTACTATGACACGGACATGGACCAGGGCGATGAGCGCTACGTCTCCATGCCCGCAGGGAAGA
 GGCTGCGGAACACATCCCTCTCTCTTCTTCCCTTCCATCAGCCAGGCTTCCAGTGGGTT
 AGGACCGATTCCAGGCCGCTCCACCATGATCATGCTCATACACCTGCCCTACGAGTGGTTT
 GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGCAGTGTACTATGAGACTTCAAAACTC
 CTTTGTGGAAGCCTCTATGTCAAGTGGTCTGAACTGTGTTCCACAGTGGAGGAGAGGTGG
 AGAGTGTGACTGCAGGATCCCACTACCAAGCTTCTATCTPGGCTGGCTCCCCAGGTGGCC
 TGCTACGGGGGCTGCCATGACCTGGGCCGCTTGCACCTTGTGTGATGGCTCCCTTAGGGGC
 CCAGAGCCCTATCCCAAGCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGCTCG
 GGGGCCGTGCAAGGTGCCCTGTCTGTGACGAGCGGCATCTGAACGGAACTGTACTACGAT
 CTTAAGAATCTTGATCTAGGATCGGGGCACAGAAGAAAAGAAAT**TAG**TTCCATCAGGGAGG
 AGTCAGAGGAATTTGCCCAATGGCTGGGCGATCTCCCTTGACTTACCATATATGTCTTTCTG
 CATTAGTTCCCTTGACGCTATAAGCACTCTAATTTGTTCTGATGCTGAAGAGAGGCTAG
 TTTAAATACAAATTCGGAATCTGGGCGAATGGAATCACTGCTTCCAGCTGGGGCAGTGAGA
 TCTTTACGCTTTTATAACATGCCATCCCTACTAATAGGATTTGACTTGGATAGCTTGTATG
 TCTCATGACGAGCGGGCCTGTGCATCCCTCACCAAGTCCCTTAACTCAGTGATCAAAGCGA
 ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTCAGCTCAACCTGGTGGGTTCAGTCT
 TGCTCGAGGCTTCTGCTCTCATTCTATTAGTGTGCTACGCTGCACAGTTCTACACTGTCAAGG
 GAAAGGGAGACTTAATGAGCTTAACTCAAAACCTGGGCGTGGTTTGGTTGCCATTCATA
 GGTTTGGAGAGCTCTAGATCTTTTGTGCTGGGTTCACTGGCTTTTCAGGGGACAGGAAT
 CCGTGTCTCTGCGCAGTGTGGTCTTGGAGCTTTGGGGTAACAGGAGATCCATCAGTTAGTA
 GGGTGCATCTCAGATGATCATCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTTATCA
 TCGGGGTGCCAGCTGTGTTCTCAATGTGCCAGCAGGAGTCACTGAGCTTCAATCAAGCA
 CTTATCCACCAATAACAGGGAAGGTGATGACAGGAGGGTGACATCAGGAGTCAAGGCA
 TGGACTGTGAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCAGGCCAAGGG
 CACAGACGGGACAGTGCAGGGAGGTGTGGGTAAAGGGAGGAGTCACTACAGAAAGGGA
 AAGCCACGAATGTGTGTGAAGCCAGAAATGGCATTTGAGTTAATAGCACATGTGAGGG
 TTAGACAGTACGTGAATGCAAGCTCAAGGTTTGGAAAATGACTTTTCACTTATGTCTTTG
 GTATACAGCATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTACATTAATAAATTTATTG
 ATTCATTGCTTTAAAAAAAAAAAAAA

09941992-08800
 109280-26460

FIGURE 64

MWLPLVLLAVLLAVLLCKVYLGLFSGSSPNPFSEDKVRPPAPLVTDKEARKKVLKQAFSAN
 QVPEKLDVVVIGSGFGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEATIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFMSHALLVNHMYKGGFYPRGSSSEIAFHTIPVIQRA
 GGAVLTATVQSVLLDSAGKACGVSVKGHLELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGLGMTSVFICLRGTEDLHLPTSNYYVYYDMDQAMERYVSMPREAAEH
 IPLLFFAFPSAKDPTWEDRFPRSTMIIMLIPTAYEWFEEWQAECLKGRGSDYETFKNSFVEA
 SMSVVLKLPQLEGGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
 PNLYLTGQDIFTGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
GGGGTTGGCACCGGCCCGGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
TGCGGTGCTGCTGAGCTTGCCCTCGGCTCCTCGGATGAAGAAGCGAGCCAGGATGAATCCT
TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAAACCAGCTTTG
ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
CGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAATGAAAATCCTTAATGGAAGCAA
TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTATTTGGTGATTACTTGCCACAGAATATC
CAGGCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAGTCAGGCAAGGCTCTTGAT
ATTATACATTTGGAGCTCTTGGGGGCAATCTAATAGCCACATGGTTTTGGAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTT
TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTCCTTCAA
ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA
ATTTTCTTTTAAATTTCTCTGAGTTGGAATTTGTCAGAATCATTTTTTACATTAGATTATCATAA
TCTTTTAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTTGTTAAATTCATGGAGTTATTT
GTGCAGAATGACTCCAGAGAGCTCTACTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC
CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
CTATTTTGCTAATTTGTACTTTTTCTTGCTAATTTGGAAGATTAACTCATTTTTTAATAAA
ATTATGTCTAAGATTAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
EPCHFPFLFLDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMGEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

094192-032401
10220-26466

FIGURE 67

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGCCTGTGTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCCATTTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQQVQLSCTLSPQHVTIRDYGVSQYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

103280.261406

FIGURE 69

GCGCGCCCGCCCGGAGACCGGGCCGGGGGCGGGGGGATGCGGCGCCCGGGGCGG
 CGATGACCCGCGAGCGACGCGCGGGCCCGGCCCTGACCCCGCGCGCGCCCGGTGAGCCG
 CCGCGCGAGGTCCCGGACAGCGCGGAGATGACCGCGCGAGCCCTGTTGCTGCTCTGCTGCCG
 CGCTGCTGCTGGGGGCTTCCACCGCGCGCGCGCGGAGGCGCCCAAGATGGCGGAC
 AAGGTGGTCCCAAGCGCAGTGGCCCGGCTGGGCGCGCATGTCGCGGTGACGTGCCAGTGG
 GGGGACCGCGCGCGGTGACCATGTGGACCAAGGATGGCGCACCATTCCACAGCGCGTGG
 CGCGCTTCCGCGTGTGCCGACAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGCTACTACACCTCTGCTGT
 GCTGGATGACATTAGCCAGGGAAGGAGAGCCTGGGGGCCGACAGCTTCTCTGGGCGTCAAG
 AGGACCCCGCAGCGACGAGTGGGACGACCGCGCTTCAACAGCCCTCCAGATGAGGCGC
 CGGCTGATCGCAGCGCGCTGGGTAGCTCCGTGCGGCTCAAGTGGCTGGCCAGCGGACCC
 TCGGCGCGACATCACGTGGATGAAGGACGACCGAGCTTGACGCGCCAGAGGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCGCGGAGACAGCGCAATATC
 ACCTGCGCGGTGTGCAACCGCGCGGGGCGCATCAACGCCACTACAGGTGGATGTGATCCA
 CGGAGCCCGTTCGAAGCCCGTGTCTACAGGCACGCAACCCGTGAACACGACGCTGGACTTCG
 GGGGACCCACGTCCTTCCAGTGAAGGTGCGCAGGACGTGAAGCGGTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGCGCGGAGGGCGCGCACACTCCACCATCGATGGGGCGGCCAGAA
 GTTGTGGTGTCTGCCACGGGTGACGTGTGGTGGCGGCGCGGAGCGCTTCTACCTCAATAGC
 TGCTCATACCCGCTGCGCGCGCAGGACGATGCGGGCGCATGTACATCTGCTTGGCGGACACC
 ATGGGCTACAGCTTCCGACGCGCTTCTCACGCTGCTGCGGACCAAAACCGCGGAGCGC
 ACCTGTGGCTTCTGCTCTCGGCGCATAGCTGCGTGGCGCGGTGATTCGCGATCCAG
 CCGGCGTGTCTTTCATCTGGGACCTGTCTGCTTGGCTTTGGCAGGCCAGAGAAGCCG
 TGCACCCCGCGCGCTGCGCTCTGCTGCTGGCGACCGCGCGCGGAGCGCGCGGACCC
 CAGCGGAGACAGGACCTTCCCTCGTTCGCGCGCTTACGCGCTGGCGCTGTGTGGGCTGT
 GTGAGGAGCATGGTCTCGCGCAGCGCCAGCAGCTTACTGGGCGCAGGCGGCTGTGTGG
 CCTAAGTTGTACCCCAACTCTACACAGACATCCACACACACACACACACTTCTCACAC
 ACATCTCACAGTGGAGGGGCAAGTCCACAGCACATCCACTATCAGTCTAGACGCGACCGT
 ATCTGCAGTGGGACCGGGGGGCGGGCCGAGACAGGCGAGCTGGGAGGATGGAGGCGGAGCT
 GCAGACGAAGGCGAGGGACCCATGGCGAGGAGGAATGGCAGACCCCGAGCGATCTGTGTG
 TGAGGCATAGCCCTTGGACACACACACACAGACACACTACTGGATGCATGTATGCAC
 ACACATGCGCGCACACGTGCTCCTGAAGGCGACGTACGCACACGACATGCACAGATATG
 CCGCTGGGCACACAGATAAGCTGCCCAATGCACGACGACGACAGAGATGCCAGAAC
 TACAAGGACATGCTGCTGAACATACACGACGACCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACCGGATATGCTGCTGACACACAGATAATGCTGCTTGCACACACATGCGCG
 CAGCTGCACAGATATGCTGCTGACACACACACGCGTGCACAGATATGCTGTGGACACGCA
 ATATTGCTGGACACACACACACACACGCGTGCACAGATATGCTGTGGACACGCA
 ACATGACAGATATGCTGCTGCTGCTAGTACACACACACGCGAGCATGCTGTCCGACAC
 GCCTGGACACGACAGATATGCTGTCTAGTACACACACACGCGAGCATGCTGTCCGACAC
 ACACACGATGACAGATATGCTGTCCGACACACACACGCGACAGATATGCTGCTGGAC
 ACACACAGATATGCTGCTTCAACATCAACACGTGACAGATATGCTGCTGGACACACAC
 TGTGACAGATATGCTGTGTTGGACATGACACACGTCAGATATGCTGTCCGATACACAGC
 CAGCGACATGACAGATATGCTGCTGGGACACACTTCCGACACACATGACACACAGGTA
 CAGATATGCTGCTGGACACACACAGATATGCTGCTTCAACATCAACACGTGACAGTGCAG
 TATTGCTGGACACACATGTCACAGATATGCTGTGACATGACACACGTCAGATATGCTG
 TGCTGTCCGATACACGACGACACATGACAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGACACACAGGTGACAGATATGCTGCTGGACACGAGCTGAGCTGGCTTTGG
 CAGGTGTGCTGCTTGAAGCGCTGAGTACGTGTGCGGTGAGGCTCATAGTTGATGGGACTTT
 CCTCTCTCCAGCTCACTCCCCAACTCTGCGCGCTCTGTCCCGCTCAGTCCCCCGGCT
 CATCCCGCTCTGTGCTTGGCTTGGCGGCTATTTTGGCAGCTGCTTGGGTGGCGGAG
 AGTCCCTTACTGTGTGGGTGGGTGGGGGACAGGAGCCCCAAGCTGAGAGGCTGGAG
 CCGTGGCTAGTGTGCTTATCCCCAGTGCAATTTCCCCCTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAACATAATATTAATATGATGGAAGGAAGATGGTGTGGAGGAC
 TGTGCTCTCTTCCGCGCGGGGACCGCTGTCTTTCAGCATGCTGATGACCAACCC
 GTCCAGGCGACACACCCCCACCCCACTGTCTGGTGGCGGAGATCTCTGTAATTTTA
 TGTAGAGTTTGACGTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

FIGURE 70

MTPSPLLLLLLPPLLGAFFPAAAAAGFPKMAKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIAFPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPV
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

FIGURE 71

CCAGCTGAGGAGCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCACGGGACCGCATTCCAGAGTC
 AGTGACTCTGTGAAGCACCCACATCTACTCTTGGCCAGTTTCCACGGGCTTGGGGGAAAG**ATG**GTGGGGACCA
 AGGCCTGGGTGTCTTCCTTCTCTGCTTGGACTGACATCTGTGTGGGGACAGACAGAT**GCT**CAACCAGTCA
 GTAAGAAGATGTCAGCCTTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTGCCAGACCCCTGGAGAGCCCTGG
 TGAGTGGACACATGGTTCAACATTCGACTACCCAGCGGGGAAGGGCAGTATGAGCGGCTGGAGCGCATTCCT
 TCTACTATTGGGACCTGTGTATGCTGGCTGCTGCTGAGGCTAGAGACATGTGCTGGACATCTGGGGC
 AGCATCGGACCTGTGTGCTGATCTCCCTGAGGGTTTCTGGTGCCTCACAGAGGAGCAGCGGCTGGCCA
 GAACTGCTCAATTAACCCGTACGCTTCTCTGCCCCACAGGATCCCTGGCGCCAGACAGAGCGCATCTGGA
 GCGCATGGTCTCCTGGAGCAAGTGTCTAGCTGCCTGTGGTCAGACTGGGGTCCAGACTGCACACCGCATTTGC
 TTGGCAGAGATGGTGTGCTGTGCATGAGGCCAGCGAAGAGGTCAGCATGCATGGCGCAGGACTGTACAGC
 CTGTGACTCGACCTGCCAATGGGCCAGGTGAATGCTGACTGTATGCTGCTGATGTGCCAGGACTCTCATGCTTC
 ATGGGCTGTCTCCCTTCCGAGGGTGCCCGAGCTCAGGGGCTCTATCTACTCTCGACACAGACTGGGGC
 CTGCTGACCCAGACAGATGTGGAGATTCGACCTCTGGCTGATGGCAAAAGCATCTCTGAA
 GATCACAAAGTCAAGTTGGCCCCATTTGATCTACAATGCCAAGACTAGCTGAAGCGAGCCACCATCAAGG
 CAGAGTTTGTGAGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCAGGAGAGCTGGGCGAGG
 GTGCTTTGTGCTGTGTGAAGGCCAGGGAAGCCAGCCAGACAAAGTATTTTGGTATCATATTAAGACACATTGCT
 GGATCTTCTCCCTCTACAGCATGAGAGCAAGCTGGTCTGAGGAACTGAGGACAGCAGGCTGGGGAGTACT
 TTGTGCAAGGCCAGAGTGAAGCTGTGGGCTGTGAGCTGAGGCTGCCACTGATTTGTCACAGACTGTGATGAG
 ACTCTTGCAACCTGCTGAGACTCTGAGACTACTTATCCGCTGCCCATGATGCTTTCAGAACTGTGATGAG
 CTTCCTATGACAGCTGGGACGCTGCCCTGTTAAGACTTGTGACGGGACAGGAGATCCAGTGCATGGCTACACGCTACCC
 ATGCTGTGCGAAGCTGCTGGCATCTCCAAGACAGAGGAAGGGAGATCCAGTGCATGGCTTACACGCTACCC
 ACCAAGGTGCAAGAGGTGTGAGCTGCCAGCGGTGTACGGAACCTCGGAGCATGTGCGGGGCGGTGTGCTGTC
 TGCTGACAAATGGGGAGCCCATGGCTTTGGCCATGTGTACATGGGGAACAGCTGCTGAAGCATGACTGCTGAC
 AGGGCACTTTGCTCCTCATGTCCCGAGGACTGAGAGGCTGCTGTCTCATATTTGTGACAGGGCTGCAGAA
 TTGTGTCACACACCAAGTCTCACTTTCAACAAGGAAGGGAGTGCCGTGTTCCATGAATCAAGATGCTTCG
 TCGGAAGAGCCCATCACTTTGAAGCCATCGAGACCAACATCATCCCCCTGGGGGAGTGGTGTGGAAGAAC
 CCATGCTGAATCGAGATTCCATCCAGGAGTTTCTACAGGACAGATGGGGGAGCCCTACATAGGAAGAATGAAG
 CGCAGTGTGACCTTCTCGGATCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGACCTGAATTCATCAA
 TGACGAGGAGACACTTTCCCTTTCCGACGTATGGCATGTTCTCTGTGGACTTCAGAGATGAGCTCACTCAG
 AGCTACTATATGCTGGCAACTGAACTGCACTTGTCTCGCCAGCTCAAGATGCCAGGACATATCCACA
 CTGAACTCTGTGCTCACTCAATCCAGACAGAGGCTGTGGGAGGAGGAAGTGTGATTCAAATTTGAAATCAAG
 GAGCAACAAGAAGAGACAGAACTTCTGTTGGGACCTGAGATTCGTGAGGAGGAGCTTTTAAAGCTGG
 ATGCTTCTGAAAGCAGCGGGTGCTTTGTTAAGTGGAGGCGCTACCGGAGTGAGAGGTTCTTGCTTAGTGAGGAC
 ATCCAGGGGGTGTGATCTTCGCTGATTAACTTGGAGCTAGAAGTGGCTTCTGTGCAACCTGAGGCTGGGG
 CGCTTTTGACAGTGTCACTACAGGCCCAAGCGGCTGTGCTGCTGGCTTCTGTGAGCTGTGATGAGCTGCTGATG
 CCTACTCGCTATGCTGTGGCAAGCTGGCTGGGGAGGAATCGAAGCAGTGGAGTCTTCTCTAAATTCACG
 CCAATGTCAATTTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCTCCGAGCGGACCATGAGGATCCAG
 GGTATAAAGACAGCTTTCCAGATTAGCATGGCCAGCCAAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCCA
 TCTATGCTCTTTGAGAACCCTCCGGGCATGTGAAGAGGCACCAACCTGCAGGCCCACTTCGGTTCTACAGATT
 GAGGGGGATCGATATGACTACACACACTCCCTCTCAGAGAGATGACCTTACAGCTGAGCTGAGCATATCT
 GGCATGTGGCCCAAGCGATGGATTTCAGGCTCTGATGAGCTGATGAGCTGATGAGCTGAGCTGAGCTGAGG
 ATGTGCAATCCCGACATGGGGGGCACTCATGGCGGACAGCTGGGGAAGCTGTATGGAATCCAGATGTGAGG
 AGCACTCGGGACAGGACAGCCCAATGTCTCAGCTGCCTGTCTGGATTCAGTGCAGTGGGATGCTCTATGTA
 TCAGACCGCTGTGACCGGCGACCTGGTGAAGGTCTATCCCCAGGCGAGCTGGCTCGAGCCAGTGTGAACCCA
 TGCTGTGATGATGATGCTGGTCAACCATTTGCCATTTGAGTCAACAAAGCAGCAGTGAATGACCATGTGCGCA
 CCTGTGGACCTGAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CGGCTCGCGGCT
 TCACCTCTCAACTCTGTAGAGAGGCAAGTAGGCGCGCAGAGTGCTTCCAGTCTCCAAAGACCCCCAGCCAG
 TCCCTCTGCTCAGGCACTGTCAAGGAAGATGCCCTCGAGGAGCAGCAGGAGCGAGGCTGGCCGAGC
 CCGAGGTGGAGTGTGGCTCTCTGATGATTTCTTAGAGTTGTCTCAACAGCCCTGATCAAT**TAAG**TTTTTGTGGT
 ACTTCAACCTCTTGTGCCCTCATTTGATGACAGCATGTGACATGATGACAACTCTGATGCTGATGCTGAT
 TTAGCCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 TTGGCACTGGCCCCCAATTTGGCACAATTAAGCCCTTTTGTGAACGTGTTCTTAAATGAACACCAAGAAAT
 GGCCATGCTTGAATCTTGACGCTTCAACTGTACTTCAATTAATGCCATTAAATGAACATATACTTCTCTCTT
 TTTGATGGTTTGTGCCCATCTGCAATAGTGATAATCTGATGCTGAAGATCAATTAACCAATATAAGGATAT
 TTCTTGGCTTGTCTCCACAGACATAGGCAAGCCCTTATCATAGTTTCATACATATAATTTGGTGAATTAAG
 AATATAAACACATACTTTACTTGAATGTAAATAACTTATTTATTTTCTTGTCTTGTCTTGTCTTGTCTTGTCT
 ACATTCAGATGAGTATTAATTAATGATCATGATGCTTCTTCAAGACTCGAAGAACATCTCTGCTGAT
 ATCCACATTAACACAGTTTGTAACTGTATTTGTACTTCTTTCCTTGTGATTCGTTTGTCTGTGATAAGG
 CCAGTGTAGCCGAGGCGAGTGTCAATAAATGCATCTCTGTATTTCGAAAAA

0041397.08267

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFFYYGDRVCARPLRLARTTDWTPAGSTGQVVHGSPREGFWCLNREQ
 RPGQNCNMYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACQGTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
 TPKLLTQTDS DGRFRI PGLCPDGKSI LKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKECSCQRCETETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGS AVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVP AFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNIAIGVPQPYLNKLNRYRTDHEDPR
 VKKTA FQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDINTVFFN
 EDDPMSWTE DYLA WWPKPMEF RACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGS CRRASVN PMLHEYLVNHLPLAV
 NNDTSEYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGS SRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

0947992-082804
 108820-269496

CTGCAAGTGTGTAAACGCGCTATACACACAAGTATGTGTAGCTTTCCACCAAAGCTCTCAATATACCTGAATACGACG
AATATCTTAACTCTTCATATTTGGTTTGGGATTCGCTTTGAGGTGCGCTTCCTATTTAAAAAAAGATACAGAG
ACCTCAATACCCGTACGTCATACATACATATGTATATATGTAAACTAGACAAAGATCCGAGATCAATAAAGC
AAGCTCTCTCTTTAGTTTTCAGGAAGATTACAAAGAAATTTAGAGATAGTTTGTTCAGAGCTCTCTGCATCTATG
CCCTTTGGGTTCAGTGTCTCAGTATGCAGCCCTACCTTTGGTTGGGGAGCATTTATGATTTCTCTAGACT
CAGATTTACACGGAGAAAGGAAATTTGGGATTCATCTAGGCTCCGACCGGAATCCACGAGCATGACAAATA
TCTGAAGTGAACCTCGATCTCCGGATATTAACCTGTGGAGACCTCTGAGACGCTCTGTGCAATGGGCATCT
CTTACATGTGCAATTAAGTGTGTATGCGATAGCTCCGCTGAGCTGGACACCCCTCGAGTGTGTTGTGATT
GAGGAAGACATCCCTCCCAATTTGGCAGTCTGCCATTTGGAAGGAGTATCCCAAGCTCTCCAGSTTAACAT
CACTCTGCTTTGGAGCAAAACATGTAGCTAACAGACACATAGTTATTAACCTTTGAATCTGGGGCTCGACAGC
AAATGATCTCGGAGAGCTCTCTGATTATGGAGAACATGGACGCTCTCAGTATTTATGCCACAGCTGCTTA
GATGCTTTTCAACATGGATCTAAATTCGTTGAAGGATTATCAGCAGTACGGTCTTGAAGAACTATTTCGACAGA
AGAGTATCAACAGGTTATACAAATAAGCAAAATTAACCTATGAAATCAAGACAGGTTGCGCTTTTGTG
CTGGACCTCGCCTACGCAATATAGCTCTCCCTCTACGACAGCTGTGACACCAAGAACTACAGAGATTTCTT
ACAGTCACAGACTCTGAGGATAGGCTGTTTAAAGCAGCGCTTGGGAAATATTTGATAGAGCTACACTTTGGC
ACGCTACTTTTACGCGATCTCAGACATAAAGTGTGCGAGGAGGTGTCAAGTGTATTTCCATCCGCTCACTGTGTG
TGTATGACACAGCAAAATGACATGCGAATGTGAGCACACACTACAGGTCAGAGCTGGGAATGACAAAGAG
AATTTATCAGGCGGCACTCTGGAGTCAGGCTCTTATCTCCCATCCCCAAGGACCTCGAAATCACTGTATCCC
CAGTATTTCCAGTATTTGGTACGAATGTCTGCGAACAGCAAGCTCTGTCAGCTCGAGAGGAGGAGCTGCCAC
ACAGCTGCGCTGCGTGGCTGCGCGGCGCTACACCGGGCATCTCTCGGAGAAGCTCGCGTCGAGGAGGCTGCG
AGCTGGCGCTCGACTCTGCGCAGGGCGCGCTCCAGCAGCGCACCCAGCTGCTGCTGCTGACAGCTGCTGT
GGGAGCCGCGCAGCCCTCGTGTGTTCTAGCTCTACCTTCAGGCCACCGGACGCGGCTGTCGCTGGGGAGCGA
GACACAAACCAAACTTGTCTACTACATAGGAAACACACATACAGCACACCCCATCAGACATGTATACAA
CTAAGAGAGCTTAAGTCACTAAGCACTATTTATCAACCGTGGACAGCACTCCGAGTCAAGACATGTTAATTCT
TGACTCCGAGGAGTGGCAGCTGTTGATATTTACTCCGTAATCAATTCAGCATTCAGAGCATATTTGTGGAG
TTGGAAAGCTGCGACAGCCGCCCAAACAGGAAGAACAAAAACAATAACCCGACCTAAAAATCAATTTGCG
TACTCTAGGCTGTGCGCCCTAGTAGCACTCCGCCAGTGTGTGGACACCAATAAGCATTTTCTGCTGAGT
GTGCAATTTGGGCATTAAGGAAATCTGTTAAACGTCGCATATTCGCTGTTCGCTCTGAATCTCCCAAC
CTGTGCTTTGTGACGCTGTGCTCTACAGCTCTGTGGTGTGTTGAAAGATTTCTTGTCTGTATGTAGTGATGACA
TGTGTAAACAGCCCCCTTAAAGAGCGAGCCAGCTCATACCCCTGTATATCTTAGACAGCTGAGTCAGTGCGGA
GCACACACCCCATATAAGAAAGTGGCTATAGGAAATGAAGGAAGTGTATATCTCTTTGTTTGAATCAAGT
ATTTTCTTGAACTACTGTATATGTAGTATTTTGTATATTTGCAATTTGTGTACACAGCAATCTGTAAAT
GTATCTAATTCGAATCAGCAAGACATGACATTTATTTGCTCTCTTCTGTCTGTGTTTGTCTGTCGAGA
GATTTCTCTGTAGGAGCAAGCAAGCTGTCTGGCATCAAGAAATACAGTTTACATATATACAGAGTGTAATAGA
TCTCCAAAGAAGCAATCTAAATTTCTTTGTGTGTAAACATGGAAGTATAAGATATAAAATCTCTGCA
TAAACGATTTCAAGAAATTTGATTTGCAATTTCTTAAGTGAAGGAGACGCGCACCAAGCATTTCCACACTCACT
TTACTGATTTCTGTGTCGAGTGAATCACTTCAGCTGACGAATTTAGTTCGAGGAGATGGATTTGATCTCACT
AGCTTGGACAACTCTCGCAAAATATGAGACTATTTCACTTGGGAAAAATATACACAGCAAAAAAAGAAAAA
AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

09944992.00001
100000.26614660

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGTCCGGCTAAGATTGCTGAGGAGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCCATGACTT
 CTCTTGTGGACCATGTCCGTGATCTTTTTGCCGTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACCTTGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTGCAGAACATTCTTTACAGGATCCAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAGCGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTCAAGTAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGT
 GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTGATCCCCAGGATTCTATTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTAGTCAGGGCAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC
 TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFQDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

0941992.082801

77/330

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

094192-03301

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCGGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTCGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGGGCTT
 CCTCCCCGCTGCTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
CCGCTTCAAGAAGCCTGCTGAGTTTACCACAGTGGATGATGAAGATGCCACCGTCAACAGA
TTGCGCTCGAGCTGTGCACCTTTACCCGTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCC
TTCTCCATCATCAGCAATGAGGTGCTGCTCCTCGCTCGGAACACTACTACATCCAGTGGCT
CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
TCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGCTTTGCTGGCTCCAGAAAG
GGTGCTCGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
AGGTATGGTGTGGGTGGCATCAGCCATGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCTTACCTCTACTCATGCATCCTTCTCTGGGGTTCTG
CTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
CAGCCCTGACCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
CTACACAGACAGGTCTGCTCTGCGACACAGAGGGTCTGCTGGAGAAGAGCGGGAAGGC
TTACAGCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTGGTGCTGACGG
GCGTGCTGTGCTCATTTGGGCCATCCACATCCTGGAGCTGCTCATGCTGAGGCTGCCATG
CCCCGAGGCATGAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
TGCCGTATTCAGGTTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTATA
GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
GGGAAGCTGTCTGTCTCCTGGTCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTTGGG
GCTCACTCGCTTGAACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
TTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
ACTGCAGCTGTGCGGCGAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCGCT
CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACAGTGA**CCTCCAGCTGGGGGTGGGA**
AGGAAAAA**CTGGCACTGCCATCTGCTGCC****TAGGCCTGGAGGGAAGCCCCAAGGCTACTTGG**
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGGACAGGCCATCTGCATATT
GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACGTGGCCT
CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
AGGTGGGGTAGGGGAGGGAAGGACTGGGCCAGGGCAGGCTCGGAGATAGATTGTCTCC
CTTGCTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGAGGGGCTTTGGACCACTG
AAAGACCAAGGGATAGGGAGGAGGCTT**CAGCCATCAGCAATAAGTTGATCCAGGGA**
AAAAAA

09441992.032801

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTCLVKFTTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

094196.08202

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

094199.132301

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCAATGCTGCTGT
GGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTC
TCATGCTGCCCAGGCTAATGTTGAACCTCTGGGCTCAAGTGATCTGCTCACCTAGGCCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTATACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

09941992.032801

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGP HAAQANVELLGSSDLLT

094192:03E01
100330:267160

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCCTCTATAAAGGATATTTAAAGGCCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGATAGTGAGAAAACGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT
 GCGGACCACCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCGGGATAAGATCACAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTCATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTAGCAATTTTCATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGT
 TTATTTTTTA

FIGURE 85

MAPQNLS^TFC^LLL^LYL^LIGAVIAGR^DFYK^IILGV^PRSAS^IKID^IKKAY^RKLAL^QLHP^DRNP^DDD^FQ
AQEK^FQ^DLGAA^EYV^LSD^EEKR^KQY^DTY^GE^EGL^KDGH^QSS^HGDI^FSH^FFG^DFG^FMG^FGG^TPR^QQ
DRNI^PRGSD^IIV^DLEV^TLEE^VYAG^NF^EVE^VRN^KPV^ARQ^APG^KRK^CNC^RQ^EMR^TTQ^LGP^GRF^Q
MTQ^EVE^VCC^DEC^PNV^KLV^NE^ERT^LEV^EIE^PGV^RDM^EY^FFI^GEG^EPH^VDG^EPG^DLR^FRI^KV^VK^H
PI^FERR^GDD^LY^TNV^TIS^LSV^LSG^FEM^DIT^LHD^GH^KV^HIS^RDK^TIRG^AKL^WKK^GE^LPN^FD
NN^IIK^SGL^LIT^FVD^FPK^EQL^TE^AREG^IQ^LLL^KGS^QV^KV^NGL^QGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGCGCGGCGGAGGAGGTTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCTGATGATCCACAAGCCCG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGCACGAGGCGGGCGGGGAGTCGCGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC
 TTGGTGCTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAAGTGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC
 TCACCTGGTGTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAG**TCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTGAGCTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAATTAAGAAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TTGGCAATTTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGCGCTGCGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAT
 ACAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCCTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLTNRNACHLTGGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

Downloaded from www.physiology.org at University of California, San Diego on 08/08/2015

GCCTTCATTTCCTCCGACTCAGCTTCCACACCTGGGCTTTCGAGGTGCTTTCGCCGTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTCTTGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTAGAAAGAACATTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTCAG
GGGCTTCTTCTGTGCTGTTGTGGCTTTATTAGAAGAGTGCCAGTCTCTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAATTTGAAGACTCATTTAAAAATATTGTGTTATTTATAAAGTCATTGAAGAATATTC
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTAAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCTCTTAGAAA
CTGTGGTGCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGCTCACTGCAATTGGCAAAAATATTCCAGTTGCCTGTATCTCTGGAAGTGA
TGCATGAATTTCGATTGGATTGTGTCATTTTAAAGTATTAACCAAGGAAACCCCAATTTTG
ATGTATGGGATTACTTTTTTTTTTNGNCNCAAGGGCC

FIGURE 90

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCN TGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTCTGTTCTTGGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

094192-06201

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCTTGAGTCTTGATCTTTCTTCTCTGGAATCCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCTGTGCCACCTGGTCTTCTGCTACGTCCTTATTGCCTCAGGGCTAATC
ATCAACACCATTACGCTCTTCACTCTCTCTCTGCCCCATTAACAAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCCATTGTCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGCTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCAACCAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
GATTCATGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCAGCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA
TAATGAAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCGGGCGGCCCTGGACCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
TGGTGCTCTACCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
GTGGCCAGCTTCATCTCTGCTTTCTTTGTGGCCTCCGTGGGAGTTTCATGGATGATTGGTGT
CAGCGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTCAACATCCGAAGGAACCTTTGGGAACTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCAAGGGGACAAGTTCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFATVRSRLNNVVSAYIDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

09041992.082801

FIGURE 94

CTGAGGCGGCGGTAGCA**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAG
 CGGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGCTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGCAAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTGAACAACCTGGGTTATAAAAC
 TGATACAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAAAAAGGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCCCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTTCCAAATTCGAATTTCTTCATTGATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACATACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACCTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCTTTTTAACCTTACAAGGAGATTTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEGEVKGAEKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASFASTPQIIKHKALDLDNRWQFKRSRLLDTDQKRKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

094199-00001

FIGURE 96

GGCAGCGCGCGCGGAGGGGAGAGTCCAGCCGAGCCGAGTCCAGCCGAGACGAGCGGACCAGCGCAGGGGACG
 CCAAGCAGCGCGGACGGAAGCGCCGCGCCGACACCCCTCTCGGGTCCCCGCGGGCGCTGCCACCCCTCCCT
 CCTTCCCCCGGTCCCGCTTCGCGGCCAGTACAGTTTCGCGGGTTCGCTGCCCGCGAAACCCCGAGGTACCA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCTCCAGCGCTCTCTTCCCTTGGCCGCGCGCTGGCACC
 GGGGACCGTTGCTGAGCGAGGCGCCAGCTCTACTTTTCGCGCGGGTCTCTCTCGCGCTGCTGGCTCTCCAC
 CAACTCCAACTCCTTCTCCCTCCAGCTCCACTCGTAGTCCCCGACTCCGCGCAGCCCTCGGCGCGCTGCCGTAG
 CGCGCTTCCCGTTCGGTCCCAAAGTGGGAACGGCTCGCGCCGCGCGCACCATGGCAGCGTTCCGCTTGGC
 CGCGCTTCTCTGCACCTGGCAGTGTCTAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAATTGCTCGG
 AAGTGCAGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCGCTCCAGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCATATTGCAAGCTGTCTTTGCTTCAAGTACAAGAGTTTG
 ATGAATTTCTCAAAGAAGTACTTGAAGTGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTAAAGATCTCTCGTAGAGTTGAACGTTTACTACGTGGTGGGAATGT
 GAACCTGGAGAAATGCTAAATGACTTCTGGCTCGCGCTCCTGGAGCGGATGTTCCGCTGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATCGCTGAGCAAGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATCGCTTGAAGATGATCTACT
 GCTCCCCTCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATATAGTGTTCAGGTGTCTCAGAAGGTTTCCAGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTTCGATCTTGAAGTGCCTTCAGTGCTCGCTCAGACCAATCACCCGAGGAACGCCAACCCACAGC
 AGCTGGCACTAGTTTGAAGCCAGTGGTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATCTGGTCCCT
 CCCTTCCGAGCAACGTTTGAACAGATGAGAGATGGCTGCAGGAAACGGCAATGAGGATGACTTTGGAATGGG
 AAGCGAAAGCAGGTACCTGTTTCAGATGACAGGAAATGGATTAGCCAAACCGGGCAACACCCAGAGGTCCA
 GTTTCAGACAGCAAAACGACATATCTCTCTCGTCAAATCATGGCTCTTCAGTGATGACCAAGCAAGATGA
 AGAATGCATACATGGGAACGAGCTGGACTTCTTGATATCAGTGATGAAAGTAGTGAGAAGGAAGTGAAGT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA
 GAAAGCCGACAGTGTGTGTGCTGCTGGGCAAGGCTACCTCCTCAGTGTCTGATCTGTTCTGCTGG
 TTATGCAGAGAGTGGAGATTAATCTCAAACCTCGAGAAAAAGTGTCTCAAAAGTTAAAGGCCACGATT
 ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAATGGCAACAATGTACAGTTTTCATATGTGGC
 CACTGTTTAAAGAGTGTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAGGAGCTGTCATTTGAGTTGGT
 TCCTGCTCCCCAAACCATGTAAACGTGGCTAACAGTGTAGGTACAGAACTATATAGTTGTGATTTGATCT
 TTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTGTTTGGGTTTTTTTCCAACTGTGATCT
 CGCCTTGTCTTACAAGCAAAACAGGTCCTCTTGGCAGTAAACATGACGTATTTCTGAAATATTAATA
 GCTGTACAGAAGCAGGTTTATTTATCATGTATCTTATTAAGAAAAAGGCCAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMAERLEGPFNIES
VMDPIDVKISDAIMNQDNSVQVSQKVFQGC GPPKPLPAGRISRSESASFARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNAGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

094192.06331

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAAGAAGC
 AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
 CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
 TCTAGTGCTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAACTGTAGCTTCTAGCTAGTGTCATTTAACCTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

AAATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGCATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRLTVVLGLLVLFITCYADDKPKPDDKPDGKDPKPDFPKFLSLLGTEIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

094499.08204

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCC**ATGG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGTCTGTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGAGGTGTGTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCATGGTAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCTCCACTACCACTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDEVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFM
WQQVFEPWTKHIGDGCCLTRETWKDLNAQFSEIQMERQPPPLKWLVPVGPIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYLLPLRGT

FIGURE 104

GTGGGATTTATTTGAGTGCAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAGTAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATGTCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATTCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTGCAAACCTGACGGAATGAAAACGACAGAATATAACTA
 ACCAACTGGAATAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACACAGAATTTGAACGTGAAGCAAGCATTCTCAG
 GAAGTCCTGGAAAGATAGCATGCAATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAACTGCTGTGGTTTTAATTTGTAACTGTGGCTGATCTGTAAATAAACTT
 ACATTTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQFIDFVPNALRHAVDGR
QEEIPVVIAASEDRLEGGATAAINS IQHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKQRNITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

094795.03661

FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTGAGCACAACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTCCGAGCCCTAACACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATTACA
 GCAGACCATCTCCGGTCCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAGAAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCGCCACCTTGGTTCAGT
 GCTGAAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAATGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGAAAGAAGAA
 CTGATATGGCTAGTTGAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAGAAAAAAGAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCT**ATG**GGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCTGTCTTGAGAAGGCCCCACCACCCAGAAAGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCCCTGGCCTAGCCTGGAGCCAGGACC**TAA**GTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAAGTGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGGCCCTCCCCTGGTCTCTCCAGTGTTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAA

109/330

FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLEPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPT

0941932-082801

FIGURE 110

GTTTGAATTCCCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCCTAAGTGAA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAAATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACCTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCT
 TTCGGGCATTCCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
 TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGTTACTTGTATTTCACAGAAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCCTCATTCTCTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGTCCAGGTACCTGTCCGA
 TGCTGCTACTGCTGTTTCTGGTGCTTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 GTGCCAAGAACCAAGTCATTTACATCTATTAAGTCTGTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCGAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCATTTTCTGTGTTTGTGTTGAT
 CTGGAACCAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACGAACTCCAGGCCATTGTGAGAT**AG**ATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTTATTCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITITLLVHIFISLVILGLLFVCGVLWWLYDYDNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFVVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSEFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

00041992.002801

[illegible]

M R T V V L T M K A S V I E M L V L L V T G V H S N K E T A K K I K R P K F T V P Q I N C D V K A G K I I D P E F I V K C
 P A G C Q D P K Y H V Y G T D V Y A S Y S S V C G A A V H S G V L D N S G G K I L V R K V A G Q S G Y K G S Y S N G V Q S I
 S L P R W R E S F I V L E S K P K G V T Y P S A L T Y S S S K S P A A Q A G E T T K A Y Q R P P I P G T T A Q P V T L M Q
 L L A V T V A V A T P T T L P R P S P S A A S T T S I P R P Q S V G H R S Q E M D L W S T A T Y T S S Q N R P R A D P G I Q
 R Q D P S G A A F Q K P V G A D V S L G L V P K E E L S T Q S L E P V S L G D P N C K I D L S F L I D G S T S I G K R R F R
 I Q K Q L L A D V A Q A L D I G P A G P L M G V V Q Y G D N P A T H F N L K T H T N S R D L K T A I E K I T Q R G G L S N V
 G R A I S F V T K N F F S K A N G R S G A P N V V V M V D G W P T D K V E E A S R L A R E S G I N I F F I T I E G A A E
 N E K Q Y V V E P N F A N K A V C R T N G F Y S L H V Q S W F G L H K T L Q P L V K R V C T D R L A C S K T C L N S A D I
 G F V I D G S S S V G T N F R T V L Q P V T N L T K E F E I S D T D R I G A V Q Y T T E Q R D L E F G F D K Y S S K P D I
 L N A I K R V G Y S G S T G A A I N F A L E Q L F K S K P N R K L M I L T D G R S Y D L F P A M A A H L K G
 V I T Y A I G V A W A A O E E L V I A T H P A R D H S F V D E F D N L H O Y V P R I I O N I C T E F N S O P R N

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCT**A**
TGCCCTTTCCGGCTGCTCATCCCCTCGGCCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGGCTCCGCGCCAGATCCCCCCCCTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCC
 TCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAAC**TAC**ACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCCTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCCGCCAGA**ACT**TATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTG
 CCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAA**CC**AACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGATCCTGGGGGCTGGGGGGTACA
 TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTGCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTCTCT
 AGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTTATTTTTTGGAGGCTAAACATAATA
 AATTGCTTTTGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVVQMYKGTVSMVPVFSLEAYWPGLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPDTLLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVLLSCPSQPFSTKLALLGQVFLDSS

094492.082801

AAAGTTACATTTTCTCGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACAA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTTCTGAAGAAAGATGGCT
GAGATGGACAGAAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCAGAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGATGG
GGGTATTCAGTGACCTAGAAGCAACATGGAGCCAGGGCTGCATAGTGTGTGAAGGCCCAGA
CATTCGTGAAGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAAGATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCTGTGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
TGCTCCTCCAGACACCTTGAAAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCA**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTTCATCCCTTCGGTCCTAAGTTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTCCCGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCCACTGAAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGGAGTGAATGTATGT
GTGCAATCGCAGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTGGGTAAAGTACAGAATTACGCAAATAAAAGGGCCACCTTGGCCAAAGGCGGTAAAAAA
AAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSFVIAFGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVGEVQGEAIPLVLALFAFVGFMILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATAACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTTCGCGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGGCC**ATG**GTGGCGGCACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGTGCGGCCGTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAAC**T**GGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCTTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACC**A**CTTTAACGTGCTCGCCTTCCCTTGCAACCA**G**TTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTGGCCGCCGACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCA**C**CGGTACTGGTGGCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGA**A**CTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG
 TGGTAGGGGCTTGGGACCCA**A**CTGTGTCAGTGGAGGAGGT**C**AGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTA**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGGTGACCAATGCAA**A**CTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTACTCTTATGCCATTTGGTCCCATCATTCTTGTGGGGAA
 AAATCTAGTATTTTGATTATTTGAATCTTACAGCAACAATAGGA**A**CTCCTGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAATGTGTGGCAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTG**C**ATATAAACCAAAAAATAACTTGTATCAAT
 AAAA**A**CTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATATTTTCTT**C**ATTACAAAAGAAATGCAAGTTCATTGTAA**C**AATCCA
 AACATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCA**A**AA

120/330

FIGURE 120

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

2025-06-19 14:26:19

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGGCCTTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTACGGGGTGACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTGAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCCTATGCATGGGTGCTCATGCACTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACAGGCTATGGAACGAGGATGTCTTCAAGAAGTGGGCTGCAA
 GGCCCTTGTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTTCTGTCTTGGCATG
 ACCCCATCAACATCCAGTTACCTCGGGGACAAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTTGCCTGGGTTCGTTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCTCATCTTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGACCTTCTGTTATGGTACCCCCACGAT
 GTTCGTGGACATTTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCACTGTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCCACAGAGAACAGTCCCGTGACATTGCGCACATT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCTTACACGGGAGG
 CCCGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGTAATGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTGCGCTGAAGGACGGGGAGGAGACCGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTACAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATCAAACCTTCGAGA
 GCAGATGGAACGACATCTAAATCT**TGA**ATAAAGCAGCAGGCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCAGCCAGTTT
 TGAGCCAGGCATCAAAATGTCAAGGAATTGACTGAACGAATGAAGCTCCTGGATGGGTC
 CGGGAACCTGCCTGGGACAAAGGTGCCAAAAGGCAGGCAGCTGCCAGGCCCTCCCTCTCTG
 TCCATCCCCACATTCCCTGTCTGTCTTGTGATTGGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

094199102201

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTF AQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVIVSDAPLPGTLLLDDEVVAAGSTRQHL DQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMTFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGE PQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDFHHTPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKI QKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATTCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCAC

094492.08201

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTCGGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCCATACCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGTAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGTCTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGTGCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTGCCAGGGTCCCGCTGTAAGT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCACGACTGTGGCTCAACCACATCTGTCAACCTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTACAGGCGAGTATCCTGCAAAAGGGGGGCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTGTGGCCGTGGCTGCTGGTGTCTACT**GT**
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTGTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTTGGGAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTTGTATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAAVTV
SLPVVRCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSRIPPLVRLPPPEPTT
VASTTSVTTSTSAPVRPTSTTKMPAPTSTQTPRQGVHEASRDEEPRLTGGAAGHQDRNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

125/330

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGCAAGCTGTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCTTTTCATTATGATTACCAGACCTGAGGATTGGGGGACTGGTGTT
CGCTGTGGTCTCTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGGCCCCAGGAGATGAGGAAGCCCCAGGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCATGCT**TAA**AAAAACCGCCACTTC
AGCAACAGCCCTTTCGCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCTCTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCACTGCAGCCTGCGGTCT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCCTTGTGGCTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAAGTGTGGACTCGATT
CCCCAGCAGGGGCTGAGCCATGAGCCATCTGCTCCCTGCCCTCGCCCTGAGCTCCATCAG
CTTTGCTCTTAGGAGGCTGCTTGTGTGCCGAGACAGCCCCCTCCCTGATTTAGGGATGC
TAGGGTAAAGACACGGGCGATGTGTCTTCACTGCTCTTGGGAACTGGGAAGTTTGCAGCAC
TTTGTATCATTTCTCATGGACTCCTTTCACTCCTTTAACAAAAACCTTGCTTCCTATCCC
ACCTGATCCCAGCTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTGAGGAGGCTATGCCCTTCCGTGGTTAATTCTTCCCAGGGGCTTCCAG
AGGAGTCCCCTATGCCCCGCCCCCTTACAGAGCGCCGGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCTGGGGAATGTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC
GTTGGGGGCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCCGTGGTCAG
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG
CTTGGAAGTGCATAACGAGAGTGGGAACCTCAACCCAGATCCCGCCCTCCTGTCTGTGTT
CCCCGGGAAACCAACCAACCGCTGCGCTGTGACCCATTGCTTCTGTATCGTGATCTAT
CCTCAACAAACAAGAAAAAGGAATAAAATATCCTTTGTTTCT

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEFQKQRTVEVQPSGGSLWNLRLRLEPLDANVDA

0941992-082804

FIGURE 128

AAACTTGACGCC**ATG**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAACTTCCTTT
CCTCAACTGGGATGCCTTTCCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAG**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACCTCCAATAAACATTTTCCATCCAAA

129/330

FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPCLKGLRSATPDAQ

00941992-002801
108280-2664460

FIGURE 130

CAGTTC TGAATCAATGGAGTTAATT TAGGGAATACAAACGACCATGGGGGTGGAGATTGC
CTTTGGCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCTCAAGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTGTTTGTGTAAAGTATTTTTTAGAATATCTGTTGACTTCT
TCATGATTTAATAACCATCCTTGCGAAGTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTGTGTATACTAGATGGCTCCATTATCCACCACCTATTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATC
TTCACCTTAATTTGTAACGATTAAAAAGAAATAGAGCAGCGAGACCTCTAGGAGAATATT
TACTCCTGGGTGCCCTGACACATTATGTAGTAGTATCCCAAAATGTGATTTGTAATTTAA
TGTTATTCATATATTAGTACATTAGTTCGTGATGTAATGAATGAACAGAGATCTATTTCTT
AAAAGTTTGTGAGTATATTTTCAACTAGATATTGTGATAGAAGACGTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

108280-2667460

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAATCTCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAATAAGTACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCTTCAAGTAAACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAACCTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCTCTCATTTCTTCTGTCTCGAAAAACCCAAACTCTGTTGATGCAGAATACACCAAAAC
 CAGGCTTGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTGTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAAAGAGAAGGAAAGGTTATGATCAAATAT
 TCCCAAATGTTGAAACTGAACTA**TAGT**AGTCATCATAGGACCATAGTCTCTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTTGTGAAATATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTTATGCAATTGGATT
 TCAGGTTCCCTTTTGTGCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLP
SAQGRQKESGSKWKVFI
DQINRSLENYEPCSSQNC
SCYHGVIE
EDLTPFRGGISRKMMAEV
VRRKLGTHYQITKNRLY
RENDCMFPSRCSGVEHFI
LEVIGRLPD
MEMVINVRDYPQVPKWM
EPAIPVFSFSKTSEYHDI
MYPAWTFWEGGPAVWPI
YPTGLGRWDL
FREDLVRSAAQWPWKKN
STAYFRGSRTSPERDPL
ILLSRKNPKLVDAEYTK
NQAWKSMKDT
LGKPAAKDVHLVDHCKY
KYLENFRGVAASFRFKHL
FLCGSLVFHVGVGDEWLE
FFYPQLKPWVH
YIPVKTDLSNVQELLQFV
KANDDVAQEIAERGSQFI
RNLQMDDITCYWENLLSE
YSKFLSY
NVTRRKGYDQIIPKMLK
TEL

094132.0334
10000.26460

FIGURE 134

CACCCCTCCATTCTCGCC**ATG**CCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCTGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCTCTACCTGGGCCTGGCTCAGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATCTCTGGGTCCAGCTCCATACCCCTAAATCTGAGTTTCAGCCA
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCTGGCACTGTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGGCCCAACCTTGCCCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAAGTGCATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRF^TSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHS^LMAAERVKA^WTSRYFGVLQRS^LYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVVP^TLGTDRLLLAFL^LTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAACTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCTGAGTGTAAGAACCTTCGGCTGCGTGTCTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGAAGTCTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGTGCTGTCACTCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGTGAAAAAAGTCTTGGTGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAATGTTGGCATTGTCTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCCTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCAACCATCAAGTTT
 GAAAGATGTTTATGTGCGGATCTGTTGAATTTATTAAAGTGAACATTCATATTCAGAAGA
 CACAAATCTTTTCTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCAATCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATGTCATATCAGTAATCTCTGGACTTTGTTAAAT
 ATTTTACTGTGTAATATAGAGAAGAATTAAGCAAGAAAATCTGAAAA

0044992.002801
 100220.26644660

MASALWTVLPSRMSRLSLKWSLLLLLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFRTLREHSNCSHQNPFVLIVTSHSPDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEK
EDKMLALSLEDEHLLYGDII RQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNLNHEKFFTGYPIDNYSYRGFYQKTHISYQEYFPKVFPPYCSGLGYIMSRD
LSPRIEMMGHVKPIKFEDVYGVICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQMLRNLTCCHY

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTTCAACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGAAATGGCTTTGTGTCGAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTCGTACTATGGAATTGTGGACATT
CCTTCTGTGGAGACCGGTGGAGAACTAAACAATTTTTAAAGCCACTATGGATTTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGGTCCAGTGGTTTTTACCATGTCAATTCGAAATT
TTTCTCTAGTATAGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNFGAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGKPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

CATTCTGAAACTAACTCGTGTCAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATATAAATAAGAGAAGAAAAA
GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAACTGGTTTGTTCACAT
CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACT
CAGATTCGGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAGGGA
TTGAATCCGGATGGAACCTCAGCCCCTTCAACCTCGGGTGGATTTCTTCCAGCTCCCAAGCC
ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAATAACCAATCTCCATTAATGTGAAGACAG
TCAAAAAGAACCTGAGGATAGACACAGCGTTCCAAGAACCCTTACAATGGTGTAAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGCATCAG
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGCCCTCGAAGACATCATAATCAT
GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCCTCA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTT
ATACAGATAAAATGCGACACTGTCTTATTTAAGTGTTTATTGTTTAAATGATGGTGAAT
ACTTTCTTAACTGGTTTGTCTGCATGTGTAAGTATTTTACAAGGAAATAAAATACAAT
CTTGTTTTTTCTAAAAA AAAAAAAAAAAGT

141/330

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

091120.264660

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTtagagtaatttctagtttggattgtaatatgaaattattttaaagggttcgct
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNNTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCTGGGTGGATTTTCTCC

GGACACGAGGCCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGGTTCTTCGCACCGCTC**ATG**CG
GGTCTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTCGAGTACCAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGCGGTGTACCTCTTCACAGAGGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCTGCTACCGGTGACCTTCT
CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCATGCGCCAAGCTGGCTATCCCGGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCTCTTCTCACCTTCCAGCGCTGCGGCTGGC
CCAGACCCACCGGAGCGCACTGACCATGCTGGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACACGTTCTCTGTCTCCCTGTTTCATCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
TTCCTGCACACGCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGTTTGTGTTGGTGGTGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCACTACCTGACGCCGCTCATCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTTGGGGCTTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCCCTTCTCCTCCGTGGCGTCTTGCCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTGCCAGCCTTTTCGGCCTCTACTTCACCAGCACTTGGCA
GGCTCCT**TAG**CTGCCTGCAGACCTCTCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCTCCAGCTGCAAGGTGGGCGCGGACTCCCC
GGCGTTCCCTTACCACAGTGCTCTGACCCGCGGCCCCCTTGGACAGCCGAGTTTGTCTGCTCA
GAACTGTCTTCTCGGGCCAGCAGCATGAGGTCCTCCGAGGCATGTTCTCGAAGCGGTATG
TGCCAGGTTTGTAGTGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

FIGURE 144

MAVLGVQLVVTLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAI RVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLC LAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVS LQYLTPLIITL NCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAA RI
AGALGGLLTPLFLRGV LAYLIWWT AACQLLASLFGLYFHQHLA GS

2941992.082304

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCG
TTCTTCCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

AATCTTCAACGAGTTCCTCTCACTGAGAAATCAGAGAGCAATATCTTCTACCGGCCCGCTGATTTCATTCAGGAGGGCTT
 AATCTCAAGAGTTCTCACTCAAAATCTTTGTGTACTACTAGTTCTGTGGGGCACTGGCAAGGTTTGTCTTAAAGAGGAC
 TTGGCTCGTTTGGGCCCTTGTAGCTGCAGAGAAGTGGCCAGCAATTCAGACACACTCTCTCGAGATAGTGAAGC
 GCGCTTCTGTCTGGTCTTGCCTTGCTCGCTCAGTCTCTGCTAACTACATTCAGCAATGGGCAACTCGACTCTCTGT
 TATTCAAGAACTCTTAAAGGTGCTTCCCTACATCGGGCTGACCAAGATAGGAAGAGCGCTCACAAGTAGCTCTT
 TCCAGACCGGTGTGGCAGCTCCAGGCCGGCTCCTCTCCGAGAGGTTTCTGACGCTGCCAACCATTCTCTTAT
 TGACAGACGAGCGCTCTGACACCACTCGACTCGTCTCTCGGAGAGGACGGGACCCAGCAATCAGCCG
 TGGACTCTGGCCGGGACACCAAGCAATAGGCCAGCGCCCTTTGAGAGATCCATATTCTTAAAGCAGATCATTTA
 AAAATAATAATGAGCTTTTGTAGTTTCTTCAAGGACAAAGAGCGGGAATGCAGTTGCCAACATCGCTCGACGCGG
 CGAGGAGAAATCTTGAAGAACCACTCGCCCTGAAGTCTTTCCAAGTTGTACCACTCATTTCCAGATGTGGTAA
 ATTACCAAGCATCAGATCAATCGAGTAGATCCAGTGAAGCGCTCTATTAGGCTGTGTGGAGGTAGCAAAAC
 CCGACTGTTCATATCATTTACCAACATATTTGTCTGTGGGTGTATGCCCGAGAGCGGGCCGCTCATGCCAC
 GACATCATCTTCAAAGGTCAACGGGATGGACATCGCAATGTCCCTCACAACTACGCTGTGAGTCTCTCTCGG
 CAGCCCTCGACGGTGTGTGTGGCTGACTGTATGCCGGAAGCAAGTCCGACAGGAAACATAGGACAGGCGCC
 GGATGCTTACAGACCCGAGATGACAGCTTTTATGTATTTCACAAAAAGTACGCCCGAGGACGCTTGGAA
 TAAATCTGGTGGCAGAGGTGGATAGGCTGGGGTTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGTGACGTTTGAAGAGATACGCTGTGTAGGCATCAATGACATGATCTTGGATTTGGCAGCGCAAGAA
 GCGGCTCATCTGATTCAAGCCGATGAAGAACGTTGTCACTCTGCTGTCCGCGAGCTTCGGCAGGAGCGGCT
 CTGACATCTTTCAGGAAGCGCGTGAACAGCAATGGAGCTGTGTCCCGAGGCGAGGAGGAGGACACACT
 CGCAAGCCGCTCCATCTGACCAATTAATTCTATCTAGAGAAGGTGGTAAATATCCAAAGACCCCGGTGAATCTCT
 CGCATGAGCGTCTCGAGGGGAGACATCAAGATAGATGGGATTTGCTATCTATGTCAATGATTTGTAGCCCG
 GAGGATGATCAAGAGCAGATGTGAAGAAATAAAAACAGTACATTTTGTGAATGGATGGGGTCTCAACTGACA
 GAGGTCAAGCCGAGTGAAGCATGGCAATTTTGAAGAAAGCATCATCTCGATAGTACATAAGCTTTTGAAGT
 CAAGAGATGATAGCCCAAGGAGACTCAGACAGCCCAAGCCGCTGCACTCAACACACATCTGGCCCCCAAG
 CGAGTGTGCCCATCTCTGGGTCTATGGTGGTGAATTTACACGGTGTGTATGATGTAAAGATATTGTATTCT
 CAGGAAGAACACAGCTGGAAGTCTGGGCTTCTGCAATGTAGGAGTTATGAAGATACAAATGGAAGAACAACTTT
 TTTCTCAATCAATCTTGTGAAGGAACACAGCAATACATGATGGAAGATAGATGTGGTGTATTTCTTCTGT
 CTGCAATGGTGAAGATACATCAGGAATACATACATGCTGCTGTGCGACAGCTCTGAAAGACTTTAAAGAGA
 ATTACTTCAACTATTGTTTCTGGCCGGCATTCTTTATAGATCAATGAGTGGGTCAAGGAGAAACAGAAA
 TCACAAATAGAGCTAAGAGTTGAACACATATTATCTGTGAGTTTATTTAAAGAAAGAAATACATTGT
 AAAAATTCAGGAAAGATGATCATCTAATGAAGCCGATGACACCTCAGAAAATATGATTCAAAAAATTA
 AACTCATAGTTTCTTTCAGTGTGGAGATTTCTATTACTTCACATCTGTTATATTTTCTTATCAAT
 AAAAGCCCTAAACCACTAAATATGATTGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCAAGGATGCAATATGGCCATTTTAAATTTACAGCTAAATATTTTAAATTCGA
 TCTGCGAAGCTTGCTTTCTTCAACCAAGTAATAATTTTTCAGAGTTAAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSFEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVD
SELSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDII LKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVSQRVQRS
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

2025.03.04.194194

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCAGGCAA**ATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGCC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCAACAATTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAACTCTGCAAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTATGTT**TAG**GATGATTAGCCCTCTTGTCTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTCCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

094395-08281
108280-267760

FIGURE 150

GGCACGAGCCAGGAAGTAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCCTACAAAGTCCTGGAAGTTTTCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCGG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTTGAGA
 GCCCCATCCTTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATCT**AGA**AATGAACC
 GTCCAGAGAGCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTGATTTGGA
 GTTCATGCAAAATGAGTGTGTTT**AG**CTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPIITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVFPFGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**ATGG**CAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTTGGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTAAATTTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTTCTGTACTGATATTAAATAAAGAGTTCTATTCCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWC AVQGQVDEKTF L
HYDCGNKTVTPVSP LGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
 CCTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
 TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
 GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
 GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
 TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
 CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
 CCACAGAACAGCATTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
 ATTGCTTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
 CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC
 TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTTCTGTAT
 CATCCTTTTCAATAAACTGTATTCATTTGAAAAAAAAAAAAAAAAAAAAA

155/330

FIGURE 155

MELIPTITSWRVLLLVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

0941992-032801

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC
 AGAAGTGCCTCCCTTTGCTCGTGCAGTAACAGTTTCAAGAGGTGGTGTGCACGCCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAATCCATCCGCGAGATTGAGGTGGGGCCCTCAACGCCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCCTTGAATACCTGTC
 CAAGCTCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAGCATCCCTCTTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTTCATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAT
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCTGCTCCCAT
 GCACATCGGAGGCCCTACCTCGTGGAGGTGGACCAAGGCCCTCCCTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACTTTTCCACGTGCTGC
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCACGCCTCG
 GCCTACCTCAATGTGAGCAGCGCTGAGCTTAAACACCTCCAACACAGCTTCTCACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCCGAAAGTACAAGCCTGTTCTTA
 CCACGTCCAAGTGTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTCAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCGACGACGACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTCTGCCCAATTC
 ATGACCATATTAACATAACACCTACAACACGACATGGGGCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTAGACCCCA
 TACCAAGGACAAGGTACAGAACTCAAATA**TGA**CTCCCTCCCCCAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGAGAGACTTTTCTGTGA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTAAGA
 CAAAAGTCAAAACA

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSNSQFSKVVCT
 RRGLESEVPQGIPTNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGA FNGLAS
 LNTLELFDNWLTVIPSGAFEYLSKRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKLEY
 ISEGA FEGLFNLYLNLGMCNIKMDPNLTPLVGLEELEM SGNHFPETRPGSFHGLSSLLKLW
 VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHHNPWNCD CDIW
 LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTG VYT CMVTNVAGNSN
 ASAYLNVSTAELNTSNYSFFT VTVETTEISPEDTTRKYKVPPTTSGYQPAYTTSTTVLIQ
 TTRVPKQVAVPATD TTDKMQTSLEDEVMKPTTIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS
 TVTAARTVEIIQVDEDI PAATSAAATAPSGVSGEGAVLP LTIHDHINYNTRYKPAHGHWTE
 NSLGLNSLHPTVTTISEPYIIQHTHDKVKQETQI

[illegible]

FIGURE 159

MELGCWTLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVV
 GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
 CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
 GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
 TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDFGGPVNGYQKITGGPGLINGRHAKIGTV
 VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
 QLYSAAFSKQKLQSAPTKKPALFFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
 WSGRAPSCIPICGIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
 RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
 ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
 VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
 WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK

FIGURE 160

ACCAGGCATGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTACTTCTGTTGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATTGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGA AAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCAATGACCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATTCCTTTTGGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTTACAGCTCATTTGTTGAGCTGAATTTTTCTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGTATCATG
 AGGGTTAAATATTTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTCTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGCAGGAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
 CAGTAGCTGAGCTGTTGCAAGTGTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAATA
 TGTCTATCAAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVLTALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGAGGAGCGACCGCGCAGTTCTC
 GAGCTCCAGTGCATTTCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCA**ATG**
 GCCCAGGCAGTGTGGTCGCGCTCGGCGGCATCCTCTGGCTTGCCCTGCCCTCGCCCTGGGC
 CCGCGCAGGGGTGGCCAGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCCCACCTTACCCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCCGG
 TCTGTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTCCCCATCACAGAGTTCTCTGGGGGACCTTGTGTCAACCAGAACACTTCCTTACC
 CTGGCCCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTCCTTCTCCTCCACGACCCGA
 GCAACTTCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCTTCGAGGACATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCCTGGGGGACCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCTCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCAGAGGTACAACCTGACCCACACCTTCAGGGACCTTGGGACTAC
 TGGTTCAGCATCCGGGCGAGAAATATCATCAGCAAGACACATCAGTACCACAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
 GTTTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT
 GGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCCAGGGCTGCTCCCGCCCTCT
 ATAACTGTCAAAACTTACACCGT**TCG**AGCACTCCCCCTCCCCACCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCCACCTGACCAGGAGGGGTTTCAAT
 TGGCTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAAGCTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCTTGCTGCCACTGCCACTGCCATTCTCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAAGAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACACA
 CACACACACAGAAATATAAACACATGCGTACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTGTTTAAGTCGGTTGCTGGGATGCACCTTGCACTAGAGCTGAAAGGAATTGACCTCCA
 AGCAGCCCTGACAGGTCTTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCACTTCTTGC
 GCCTTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTTGGATGGGGGGCAGGACT
 AATACTAGTATTGCAGAGTGCTTTATAAATATACCTTATTTATCGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGGG
 TGGCTCAGCCTGTAAATCCAGCACTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCCCTGGCTAACACGGTGAACCCGCTCTACTAAAAAAATACAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCCAACCCGGGAGGCGAGCTTGCACTGAGCCAGATGGCGCCACTGCACTCCAGCCTGA
 GTGACAGAGCAGACTCTGTCTCCA

108280-26614660

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTSASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVGVHPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDIVVTTQNTSLWPSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIGFTVTKLVVAEWEVEEPDATRAVKQKTGFDSASLKLQETLRGIQVL
GPTLTIQTFQKMTVTNLFLGSPPLTVCWRLKPECLFELEGECHEPVSASTAYNLNTHTFRDPDG
YCFSIARAENISKTHQYKQIWPSRQIPAVFAFPCEALITVMLAFIYMTMLRNATQQKDMV
ENPEPSSGVRCCCMCGGPFLELTPESEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAAC TTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCAGAGGCGAAGGAGCGAGACACCCACTTCCCCTCTGCATTTTCTGCT
GCGGCTGCTGT CATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCAGAACATAGGTCTTGAATAAAA
TGGCTGGTTCTTTTGTTCCTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCKT

2025-26-7-66

FIGURE 166

CTGTCTAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTCACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGGCTGGGCTA
 CCTTGAGAAATGGAGCGAGGAGCCAAAGGAGAAGAACCCAGCTTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTCTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGCCACGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTCAGAGAGCCATGGTGAAGGCCCTG
 CCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCCCTCAATTTGGCGATGCCTTCTGGAAACAGCAGCAAAATACGGGA
 TGGTGACGTACTGCTGCCAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGCGAGATGAAGATGCTGTCCAGTTTGCGAATAGGTTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAGAAGCTGTACAGCAAGATGATCGTGGGGAACCCAC
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGGCGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCGCCACTGCTGTGTCCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCAGGACTCCGGCTTTCGCCGAGGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACCGATGCTGCTGGGTGTGCGACCCAGGA
 CGAGATGCCCTTGTCTTTTACAAATAAGTCGTTGGAGGAATGCCATTAAAGTGAATCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGTGCTTGTGCTAGAGAT
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGGCGGCCACCG
 CTCTCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGTAAGGCTTAACCTGAACTCCCC
 ATGTGATGCGCGCTTGTGTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAAATGGTGGTGAATCTACTCACAGGCTGTTGTGGGATTAAGATGCTGCGGGTGAGTGA
 AGGACACATCACGTTCACTGTTTCAAGTACAGGCCACAAAAACGGGCGACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTGGATTGTGTTCTGTGAGTAAATAAACTGGCTGGTGA
 TGA

09941997.062601

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSKSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRNYNFQYISRLTVLWGLGVLIRYCFLLPLRIALFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSR

GCCCTCTGAAACCAGGACTCCAGCACCTCTGTTCCGCCCTCACCCGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCGCTGCGCGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCACCATCTGCCCCTGGGCCTGGCTCCAGACACCTTTGA
 CGATACTTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAG
 AAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
 CCGCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAAGGCAGTGGCCCACAGATTGGGGAGAAGAGGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCGCCCCCTG
 GAAGACTCTGCTCTTGGCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACTGGTTCCGGACCCAGCCTTAGACCTTCTCCCCAACAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTGTGCTATGTGATGGGGACTTCCT
 GGGACAAGCAAGGAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPFGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLLAPGEFQLSGVGP

D94192.08201

FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAACTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTGGTGCCCCCT
 CCTGCTCAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAACTCCTAACATATGCCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
 TCCAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
 CACTCCCTAAGTCTCTGCTCA

094792.08201

171/330

FIGURE 171

MAGSPTCLTLIYILWQLTGAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDEVITWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTHEYDTIPHNTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

09241992.082801

CTTGGTTCCCCAACATGCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTGAGCAGAAACCTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTGCTT
GTGTCCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGACAAGAAGAGATGGACATTTGTGCGGAA
ACTCTAACATATGCCCCCATCTCGGAGAAACACAGACTACGACACAATCCCTCACACTAA
TAGAACACATCTAAAGGAAGATCGGACCAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAATAATCCCCACTCAGTGCTCAGCATGCCAGACACACCAAGGCTATTGTGCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

GAAAGACGTGGTCTGACAGACAGACAATCCTATTCCCTACCAA**AATGA**AGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCCTTGACAAAAGA
GAAAAGATAGAAGACATGGCAACTTTAGACTTTTTCTGGAGCAATCCATGTCTTGGAGAA
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTTATCCAAT
GCCAATCGTGCCTCCAGGCCGAGAATGAAGAATGGCTGAGCCCTCCAGTCTTAGGTGAGGAC
ACTTCTCACCAGGACTCCACCATTCACTCCCTTCCTATCCATACAGCATCCCGAGTATAAATTC
TGTGATCTGCATTCCACTCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACATCATCAAGAATCAAGAGCTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT
TTTTCATGAAATTATTCCTCTTCTGTTCAATAATGATTACCCCTTGACACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVHTVVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSEIKERFAQLCEEHGILRENIIDLSNANRCLQARE

094492-08201
103280-2667460

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
TGTGTGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAIAAAAAAAAAA

176/330

FIGURE 176

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSCLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

094192-08301
10320-267460

FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAAA**TAGT**GAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

100220:263160

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

0944992.082801
T08280.264460

00000000000000000000000000000000

00000000000000000000000000000000

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

0944992.082801

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCCGCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCCTCAGCTGCCATTGCACCCAAGGATAATCTTTCATCAGTTCCCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCGTCGGATGCTGAC
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTCAGAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCCTGGTGATGACTTCACAGACGCTGTTCATCCGGGAGCGGCGTGG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTTCGAGGCACCCAGAATACCAAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGCGGGCTTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCA
TGACCTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFCPPKRNWFWG
HGLITPTEEGLKDSTQMSATYSQGFVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDFFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

00047362-00001

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAAC TCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACC CAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATA CA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACCCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCTGTTTATTGTTACCTGGAAAATAAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAAAAA

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGTTTAAAACAAACGCCAGTCATCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGCTCTGCAACCCAGCTGAGGCCATGCGCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTTGAGCCCTGAAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCAGCAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCAGCAAGTCAGTCGCCACAAAGCCTTCACTCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGTTGCTTCTGCAGCAACTTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAACGTGA

186/330

FIGURE 186

MPSPGTVCSLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

094192-082503

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCGTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTCTGCTGGACTTTCTTGCCCTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAAGGTCAGCCTCTCCAGAAAGTGAGATCATGGACAAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCACAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCCTAACATGAAATATATTACAGCAGGTCACCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTTATAACACAGGTTACCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAAAACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

00041972.002501

GGAGTGCAGATGGCATCTCTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
ATGGAGCTCTCGAAGGCCCTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCCGTGTCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
GATGGAGATACCAACACATCCACCAGGAGGTGGTACAATAACAAGTGGGAGACTGGGGATGA
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAAA
GGACTACTGGAATTTGCCAGTTTGAAGGCCATGTCACCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAAATCCTA
TGGTTATCCCTGGGAACGCAGATCAGCTACATCGGACTTCAATTATCAGCTTCTCCTGCT
ACTAACAGACTTGCTACTCAGTGGGAACCCCTGCCTGTGGGCTCAAATGAGCGCCTTTGCTG
CTGTTTCCCTGTGCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACTGTGTCATGGCGTGGCTGTCAACACCTTCA
ACACGTACACCAGGATGGTGTGAGGTTCAAGTGCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAA
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGA
GTAGGCTTGAGCCCTACCTTACACGTCCTGCTGATTATCAACATGTGCTTAAAGCAACATCCG
TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGTTATCTTTAAGTC
CTAAGGATTTCTGGGTGCCAGTCTCTCTTTCTCTACAGCTCCATCTTGTTTACCCAC
CCCACATCTCACACCTCCAGAATTCCCTCTCTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
TAAACCATGGAGATAAAAAAGAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEYVQYNWETGDDRFSEFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSCQLGSRRLTETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

0994992.082804

AAC TGAAGGAAGAAAGAAAGAAAGGT CAGCTTTGGCCCA**CATG**TGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTGCATCTCCCTCACTTAAGTCTCAGGCCGTGCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCAA
GTCGTCTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGAGATTACCATGCAAGCGCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCTTCCCTTCCCTGCCCGCCGTAGATTAG
GACATTGCCCTTGTGTGCCACCAAAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTATCGGAAAGATCATCTGCTGCATGATG
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTCAGGCTGTGAAGGAA
ATAGAACAGTCTGCTGGGAGTAGCACTGGAATCTGATTCACCAACTCTTTATTACTTTGGG
AAGTCACTCAGCTGCCGTAGCCATCTCTCAGGCTGACGGAAACCAAGTGATTACCTGCTGG
AACCAAGGAAACTAACATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAATAATCTCTAACACTGAAA

192/330

FIGURE 192

MWLPLGLLSLCLSPILSPILSSPSLKSQLACQQLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

09941992-082801

FIGURE 193

STAGCGCGTCTTGGGTCTCCGCGCTGCCGCTGCTGCCGCCGCCCTCGGGTCGTGGAGCAGGAGCGACGTCA
 CGCGC**ATGG**CAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTGTATGCTT
 GGATGTGCCCTTCCATATACAAACAACTACTGGCCCCCTTTGTCTATTATTTTACATCCTTCCACCTATTCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTGTGAAGGAACCTTGCACCTTTTC
 TTACACCGGGCATTGTGCTGTACGCTTTTGGACTCCCTATTGTATTGTCCAGAGCACATCTGATTGAGTGGGGA
 GCTTGTGCACCTTCTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGT**CGA**AAAGAAATTACTGAACATATTGTCAAATGGACTTCCGTGCATT
 GTTGCCCATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTCTGTAAGGATTAAAGGATTTTCT
 CTTTGGAAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGGTTGATTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTAATGTAATCA
 TTTGCAATGGTTAGGAATTGAGAAATCCGCCGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATTTAT
 TAGCCTCCATTATTAACAAAAATATAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTTATAGACTGTATCTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTAGAAGAAATTTATGTTAACTTTA
 AGGTAAGGGTGTAAAAACATTTTGGAGTAAGGTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTTACCTGTAAAAATGGACATACATGGAACCACTACTGATGAGGGCAGTTGTATGTTTGC
 ATCATATATGCGAGAAAACCTTCTCTGCTTCCCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 CAGCTTTTCAAATATAGTTTAAATAACACTAGAGTGTTTACTTACCTGGAAAATAAATGCTATGCCGTACATT
 TAGAGTGCCCCCTCCCTCAGGCCCTTGCCATGATTAACAAGTAACCTTTGTAGCTTACAGATAAATCATGCA
 TTAACAGTTTAAAGATTAGACACCTGGTAATAGTAGTCTTATCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTAAAGCAAGTTTCTGTATACCTCTGAACCTGTTTGTATTGTTGCTGCTTTACATCATATAGATCTGCTGTT
 CCTTATAAAGGCATTTGTTGTGTAGCTTAATGCAAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCCAAGTACCGGCATGATCAATTTATAGTGTCTGTTACATCTAATTAATATCAGGA
 CTTTTTTCAGGAGTGGGTATATAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGATATTTGTTGTATG
 TTTATTGAGTATATACATAAAAAATTTTCCGCATCAGCCAAACCTCAATCATGACAGCTGTCTGTGT
 TTTATGAAGTTATTTCTCAAGAAAATGGGAATAAAATTTGGGATTTGTTGAGCTTTTACTAAAGATGCCATA
 AGCCACAGGTTTTATTGCTCAACTTAAGCCATGACTTTTATGATATGAGATGACCGGAACGACGACGAATATCG
 CGGTGTGGCTGGAGCCTCCCACTGGAGGCTGAAAGTGGCTGTGGTATTATTAATGTTACAGATTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTT
 TTTTTGCAAGAGTGCACTTCTCGGTCCTTCCCTATTCTCTGTTCTGGATGCTGTCAGTGCATGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTTGCATTGGCAGCAT
 GTGCTTTGACCTTTGTACTAGCTTGACATAGTGTGCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGAATATGCACTGTACATCAACATTACCATTCTTCTATGGAAGAAAACCTTTGATGATGAAACAATTA
 AGATTTTAAATATCTATTTTAAAAAAA

194/330

FIGURE 194

MAGIKALISLSFGGAIGLMLGMLGALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAGFLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

0941392.00001

FIGURE 195

CCACGGGTCGGGCCACGGCTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCC
 CACGGTCCGGTGCACCTCCGGCCACACCTGCCTGGTGGAGGGAAGAGCGCCGGCGCTCTCGCGCTCC
 CGCGCGCGCGTCCGCACTCCCAACCGCCGCCGCCGCCGCCGCCGCAAGCATGAGTGAAGCCGCTC
 TCTCGACGTCCGGGGCGCGAATGGCAGGCTGTCTCCGCGGATAAAGGTTGGCGCGGTGAGTGGTCTGCTT
 CAATGACGCACATTAAACAGACTGTCAATCCTGGGGAGTCCGAGGCCCGAGTTTGGAGTTTTCGCCCCAC
 AACGTCACAGTCCGAATCCGAGAGGAAGGAGGGCGAGAGGCGAGTCTCGCGCTCCGCCACGTAGTTGG
 GAAACTTTCGGGGTCTTGAAGTCTCCGCCGCTTCGCCGCCGCCCTCGACGTCGCGCGAGCAGGACGAAGT
 GAGACATTGTGGGCTCTCCGATTCGCCGGCCGCGACCGGGGTGCTCGGAAACACAGAGGGTCTTCTCTC
 GCGCTGCATATTAATAGCTGTGCACAAAGGGAGCAGCTGAATGGAGGTTGTCACTCTCTGGAAGAGATTCT
 CACCGAGCGGCTTCCAATGGACATTCTCAGTCTCTCTGGAAAGATTCTCGATATGCTGCTGCTGCTGCT
 CTCTGTCTATATGCTGCTGTGAGGAGGCCCTCGGGGGTGGTCTGTCTGTCTGCTGGGGGCTCTTCAGTGT
 GCCCGCGCGCCGCCACACCTGTCCGGGCTGTGGGCTGTCCCTGCGCTACACACGCTCTCGGAGTCCGCG
 TCACCGAGGGGCCACACACCTGTCCGGGCTGTGGGCTGTCCCTGCGCTACACACGCTCTCGGAGTCCGCG
 GCAGCGCTTTCAGAAAGTGGCCGAGTTAAGGAACCTACGCTGAGTTCCAACACAGATCAOCCAACTGCCCAAC
 CCACTTTCGGGCCATGCCAACCTGCCGACGCTGGAGCTCTCGTACAAACAGCTGCGAGGCGCTCGCGCCGAC
 CTCTTCACGGGCTCGGGAAGCTCACCACCTGCATATGCGGGGCCACGCCATCAGTTGTGTGCGGTCCGAT
 TCTTCAGGAGTTCGCCAGGCTCAAGTTCTCGACATCGGATCAATCAGTCTCAGAGTTCGGCGGCAACTCTT
 TCGCGGCTCTTAAAGCTCACCGCTCGCTTGTGCGGAGGAACAGGTTGGCATTGTGGTCACTGCTGGAGCT
 CGCGCTCATCTCTGACCTCGCTTGTGCGGAGGAACAGGTTGGCATTGTGGTCACTGCTGGAGCT
 TGCTTTGAACTGGAGAAATGGACTTGTGCGGCGACGAGATCGAGTACATGGAGCCCATGTGTTTCGAGACCG
 GCGCGACCTGCACTCCCTCGAGCTGGACTCCAACCGCTCACTACATCGAGCCCGGATCTCAACTCTTGG
 AAGTCCCTGACAAGCATCAOCTGGCGCGGAACCTGTGGGATTTCGGGGCGCACTGTGTGCGCTAGCTCTG
 GCTCGCAACTCTCAGGGGCTTACGATGGCACTTGCAGTGCCTGCCAGCCGAGTGTGTGCGCTAGCTCTG
 TCTGAGACCGCTGTACGCTTCCAGCTGTGAGGATGGGCGCACCACCGGCCCACTGTCTCGCGGAGG
 GTCCACACCGAGTATGATTCGGGCGCCCTGCCAGCTCGGCGCACCAGCTCGCGGAGCGGGGAGGGGACGA
 CCAAGGACATTCGAGCTGCCACTGGCTTGTTCAGGCGGGGAGCAGCGCGAGAACCGCTGACATCTCACA
 AGGTTGCGCGGACCACTGCCCTCATCTCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 GTTTCGCCAGCAOCTCAGGAGCTCAGACAGTGTCTTTCAGCAGCGCGGAGCAGCGCGAGAACCGCTGACAT
 CATGATCAGATGGCTGCCATGTCTGCCGAGGATACAGCTGTGATTAACACCGCAOCCATTCAGGAGCGCC
 TGGTATCTCAACAGATATGCTCTGTACTGCCACAGCAGCCGCGAGGGAATGCGAGGTGTGATTGTGCTG
 CAGTGCTCTCAACCGCTGCCCTTACCAATAACGCTGGCGGAGCGGCGGCGGCGGCGGCGGCGGCTGGGGT
 CTCTCTGTCTGCTCTGATATGCTCTTGAATGAACTTTAAGGGGATCTCTCCGAGAGACTTACATATTAG
 CTATTATTGTGCTCTTAAACACAAAGCGAATTAACACACACACAAACCCAGCCACACACTTCAGGACCT
 TATCTTAAATTTATATGAGAACTCTTCTCTCTCTTGAAGTATGCTTCTTCTTCTTCTTCTTCTTCTTCT
 AAAGTGGCCATAGACAGAGAGGATTAATCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 AACATCATGTATGACAGACTTTAAGTCCATACGATTTCATGAGAACCATTTGAAAGAGGAAATCGCAATC
 TGGGAGCTTAAGAGCAATGATGACCATAGAAAGCTATGTTCTTACTTTGTGTGTGTGTGTGTGTGTGTGT
 TTTGTGTCTTTGTAGGCAAGCAACGTTGTCTACACAAACGGGAATTTAGCTCAGATCATTTCAATGCCCTGT
 GCTCTAGCTCTGGAGATTGGTGGGGGAGGTTGGGGGGAACGGCAGGAATAGGGGAATGTGAGTTTAAAT
 AAGGTTTTGTAACATTGAATCTTTTCTTCTTCAAAATTTATCTTTTAAAGTGTAGCACCTTTTTTTTATCTC
 CCTTAAGCAACTACTAGATTCTTATGTCTGTGTATCTGAAAGAACTTAAGGCCACATTCAGCTCTGCTCG
 CACAGAGGGTGTATCTTATCTATGTCTGTGTATCTGAAAGAACTTAAGGCCACATTCAGCTCTGCTCG
 GGCATTGTGATGGAATGACCTTCATTGTGAGTACCTTCCAGTGTATTAAGTTCAGAGTGGTATTTGAGTT
 TTTGGAATTTATATAGAAAAAAGTCTTTTACATGACAAATGACACTCTCACACAGTCTTAGCGCTAGTA
 GTTTTTTAGTTTGGAGCAGGAGGAGTTAAATGAGACTTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG
 CCGTGATGCTCAGATCTAGCTCTGATATTAATCTGAGCACTCTCCCAATTCAGCTTACAGCTTATCTCC
 ACTACAAAGTATCTGCAAGCAAGTCTTCCAGTAAAGGAATAGTTTCTTCAACATTTAAAAATTT
 TCTTCTGAACTCATCAAGTAGAAGAGCCCACTTTCTCTGCTTCAAGAAGCGAGCATTTGGTATG
 ATTATGACATCAACACATTTTATGATATATGAATATCAGAGGGGCAATGCCATCTGTATTCTTCTTCA
 AGTTTTCAGGAGTACACAGACTCTGTGTAGGATTAGGGGCACTTGTGTTTCGGCTTATTTAGTCTGCA
 CTGTGTCAGAGTTTGTGCTTGTCTCTGACATGCGGCTGAGCAGCAATTAACAGGACCAAAATATATCTG
 GGTAGAGAACTCATCACTTCCCTCAGCAAGAAATTAACAAATAAATTTCTCTCTCATGTGAGTGGCGATTG
 AGCAGCTGTCTATCTTTCAGGCTGTCAAATAAATTAATTTCTCTCTCATGTGAGTGGCGATTGTG
 GCTGATTGGGTCTGCAATTCAGAGATGTCAAATAAAGGAATTTAGCTAGAATATGACCAATTAATGTGCT
 CTGAAATATTTTGAATAGGTTTGAATGTCA

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQFTGLMQLTWLYLDHNNHICSVQGDADFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLHENDLVKVNFAHFPRILISLSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEI EYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGA EPTSG
HLLSAVTNRSDLGPPASSATT LADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYGSCTCHQQPARECEV

D 544331 03201

GTGCAAGGAGCCGAGGCGGAG**ATG**GGCGCTCCTGGGCCGGGTCTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCTCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGCGCGCTTGAGTCTCCCGCGGACAAGATGG
TGTCAGTCTCTGGTGAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGTGGATGGGGAA
CTCGTCTGGCTTCAGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACTTGGACTGTGG
CGCGGGCGAACCCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCTGGGGCTTCGCCCTGGCGCTAG
CCCCGTGCGTGTCCGAGCATCTCGGCTCTGGGCGCGACGTTACGCGCGACGAGGACCTGG
CTGTTTCTTCTGGCGTCCCGCGCGGCGCGCTACGCTTCTCAGGGCCGGCGCGCT**TGA**CGCGTG
GGCCCCGAGGACTGCGCGGACCCGCTCGGGCTCTGCGGCAACGCGGAGGCGCAGCGGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

198/330

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLVLSAGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

0941992.082804

[illegible]

200/330

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

0941942.082804

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCCTCCAGTACCCCTCCCGCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCTCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCCAGGGT
 GGGAGAGAAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTTACACTG
 AACTGATCAAGTACTTTGAAATATGACTTCGAAATTTATCTTGGTGCTCTCATACTTGTCTGCACGTGAGTCTTTC
 AACCACTCTTTCTCCCACTAGACCAGCAAAGGTTCTACTAGTTCTTTTGTATGGATTCCGTTGGGATTACT
 TATATAAAGTTTCCAAAGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACTACCCTTAACCATTATACCTTTGGTAACCTGGCCTCTTTCAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCCGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAAGTTT
 GGGAAAGCGACACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTCAGCCATGTGGCCCCGA
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAGAGCCCCATAATCTTGGTCTTCTCATTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCGCTGCATTTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCGAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCACTACCTGGATAAAGACCACTATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCTTCCAGAAAGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCTAGCAGTGGCTGATGAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTCTGTAGGCAACC
 ACGGTTACGATAATGGCTTAGCAGATATGCATCCAATTTTAGCCCATGGTCTGCCTTCAGAAAGAAATTC
 TCAAAGAAAGCCATGAATCCACAGATTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTCGAATGTCAGGATCTGCTCAATTGCAAGTGAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGGTAGTGTAAACAGCAGAATATGACCAAGAGGGGTCTACCCCTTATTCATAGGGGTG
 TCCTTGGCAGCATTATAGTATTGTTTGTAAATTTTCATTAAAGCATTTAATTCACAGTCAAAATACCTGC
 CTTCAAGATATGCTGCTGAAATAGCTCAACCATATTACAAGCCATAATGTTTACTTTGAAGTGGATTTCGATA
 TTGAAGTGGAGATTCCATAATTTATGTCAGTGTAAAGGTTTCAAATTTGGGAAACAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATAC
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTTCTTCACTGTAGCATAGGGATAGATAAG
 ATCTGCTTTATTTGGACTTGGCGCAGATAAIGTATATATTAGCACTTTGCACTATGAAAGTACCTTTATAT
 ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAAITTTGAATGCACCTTTATGGACAGTTATGCTCTTATAAC
 TTGATTGAAATGACAACCTTTTGACCCCATGTACAGAATCTGTTACGCATTTGTTCAAACCTGAAGGAAAT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTTGAGAGAAGAAGGTTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCACACACAGAAATGCACTCTGSGCAT
 TTCTTGTCTTATTTCTTCCAGAGACGTGGTTTCATTATTTTCCCTCAAAGAGTCAATACTGACAG
 ATTCTTCTAAATATATTTGTTCTGTATATAAATATTGTGATTTCCTGATGAGTCATATTACTGTGATTTTCA
 TAATAATGAAGACACCATGAATATACTTTCTTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACAGGCA
 CCATCTCAGCAATGTTTCTCTTGTGTAATTTTGTCTCTTGAATTAATTTGCTCCTTGAATTAATCACTATTAA
 AATCAATTTGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSVFILAALSLSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVWFWSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTEIDQSPVAAILPKEGKFDEVYEALTHAHFNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHLIQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG
 GACAGGCCCACCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCCCTGGGTCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCCAACAGGGACATGCGCCACCTGGGACGAAAAGGCAGTCACCCGACGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTCACGGTCGTGGGAGACGA
 CTACCATGCTCGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGTTTTAGGTGCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGACATGAGTTTGTCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

05049500

0967-806X(199609)14:3;1-B

[illegible]

GGGCTCGAGCTCGAGGCGGAATCGGCTCGAGGGGCGAGTGGAGACCCAGCAGGGCCGCCAACAAT
GCTCTGAGTGTGCTGCTGTACGTCGGCGGTCACTCGGGAGAGGCCACAGCCAGTTTCCAGTACATTG
 AGTGCAGAGGGGGTCCGCGGAGCTGAAGTCCATTTTTCAAGCTCAGTGTCTTCTATCCAGCTCC
 CAGGAATATCTCCACATACGCCAGCTGAGGAGCAGAAAAATGTACAAGCTGAGATTAAGGACCT
 TGATGGGAGCTAGACTTTGAAGAAATTTGTCATTATCTCCAAAGTATCATGAGAAGACCTGA
 GGCCTGGTGTGTGTAAGATTTGGGACAAAAGATATGTAGACCATGTAGCGCCAGGAGATCAT
 CAGTCCCTGCGGGAGTTGGGACATCAAGATATCTGAACACAGGCCAGAAAAAATTTCCAAAG
 CATGGATAAAAAAGCGCACATGACATCTGACTGACAGCAAGTGGAGAGACTACCACCTCTCC
 ACCCCGTGAAAAATATCCCGAGATATCTCTACTGGAAGCATTTCCACGATCTTGTGATGT
 GGTGAGAAATTAACGCTCCGAGTGAAGTGCAGTGAGGAGGACGGGATGTGGT
 GAGACATCTGAGTGGCGGAGGTGGGGCAGGGGCGGTATCCGAAGATCTGCACGCCCCCTGG
 CACGGCTCAGGTGCTCATCAGGTCATGCTCCCGACCAACATGGGCATCGTTGGT
 GGTCTACTCAGATGATTGAGAAAGAGGGGGCGAGGTCACTCTGGCGGGGCATTTGGCATCAA
 TGTCTCAAAATTTGCCCGAATCAGCCATCAAAATCATGGCTATGACAGATTAAGCGCT
 TTGTTGTGTAAGATCCAGGAGACTTGAAGATCAGAGAGGTTGTGGCAGGCTTTGGCA
 GGGGAGCTCCCGCAGAGCAGCATCTACCAATGAGGTCTGAAGACCGGATGGCGCTGG
 CAGAGCAGGCGAGTACTCAGGAATGTGGAATCGGCCAGGAGGATCTGGCCAGAGAGGGG
 TGCTGGCTCTTCAAAAGGCTATGTCCCCAACATGTGGGCATCTCCCTATGCCGGCAT
 GACCTTTGAGTCTACGAGAGCGCTAAGAATGCTGGCTGCAGCACTATCGAGTGAACAGCGC
 GGACCGCGCGTGTGTGTCTCGGCTGTGGCCATGTCCAGTACCTTGTGGCCAGCTGG
 CAGCTACCCCTTGGCCCTAGTCAGAGCCGGATCGAGGCCAGGCTCTATTGAGGCGCT
 CCGAGGTGACCATGAGCAGCTCTTCAAAATATCTTCGGCAGCAGGGGGGCTTCGGGT
 CTACAGGGGGCTGGCCCCAATCTATGAAGTCTATCCGACTGTGACATCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTGGGCGTGCACTCGCG**TGA**CGGGGGGAGGGCGCGCG
 GCGTGTGACTCGCTGATCTTGGGCCCGAGCTGGGGTGTGCAAGCTCTATCTTGTGAAT
 AGCTCACTAAGCTCTCGACCAAGCTGTGAAAAACTTAGACGACCCGAGGAGGGT
 GGGAGAGCTGGCAGGCCAGGGCTGTCTGTCTGACCCAGCAGACCTCTCTTGTGTTGT
 AGCGAAGACCAAGCATCTCTTAGGTCAGGTCAGCAGGCTCGGGCTCATAGTGTAA
 GGACAGACATTTCTGCAAGTGCCTGCCAATAGTGAGCTTGGAGCTTGGAGGCCGCTTGT
 TGTCCATTACCTTCAGCCAGCTGTGGCCAGTGTGGCCCGCTGCCCTGTGTCGTGT
 ATCTCCCTGTGCCCTTGTGTCGCTGCTGTCTGTGAGGTAAAGTGGGAGGGGCTACAG
 CCCACATCCCACCCCTGCTCAATCCCAATCCATATGAAGGTGAGGTACGTGGCTCT
 CCCAGGCTGACATTTCCAACCTACAGCATTAGCCCAACTTGGCTGTGAAGGAAGGAAAG
 GATCTGGCTTTGTGTCATGTCATGTAGCTTGAGCCTGTGATGCTGGGCTCTCGGGCATGCT
 TGGGACTGAGGGGGCTCGGCTGCTGGCTGGCTGCACAGAGGCAAGTGTGGGGCTCA
 TGGTGTCTGAGCTGGCTGACCTTGACCTTCAGGATGGGGCCCACTCAGAACCAACTCAGT
 TCCCACTGTGGCATGAGGCGAGTGAGCCAGATGTTTGAAGGCGAAGGCGAGGCGTTGT
 GTGTTCTGGGGAGGGAAGAAAGTTGTGGAGGCTTAATTAATGACTTTGGGAAGAGG
 TTTTGTCCAGAAGGACAAGCGGCACAAATGAGCGACTTCTGTGTTCTCAGAGGAAGACGAGG
 GAGCAGGAGCTTGCTGACTGCTCAGAGTGTGTTCTGAGCCTGGGGGTTCTGTCCAAC
 CCAGCAGGGGCGAGCGGGACGCCCCATCTCACTTGTGTCAGTCTTGGAACTATT
 ATTTTGAATTTATTTGAACAGAGTTATGCTCTAATCTTTATAGATTTGTTTAATTAATA
 GCTTGTCAATTTCAAGTTTCATTTTATCATATTTATGTTCATGTTGATTGTACCTTCCC
 AAGCGCCCGGATGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGCCGCTGAGTCACAT
 CTGCTCAGAGAAATTCCTTTGGGACTGGAGGCGAGAAAGCGGCCACGAGGACAGCCGCT
 GCTCTTTCTTTTGGCAGGTTGGGGAAGGGGTGCCCCAGCTTAGGATCTCAGGTTTGA
 CTGGGGGCTGGAGAGGAGGAGGAGGAACCTCAATTAACCTTGAAGTGGAAATCCGATTTATTC
 CTGGCTGCGAGGGTGTCTTTATTCACCTTTTCTGAATCTCAAGCGAGTGAAGTGCTTC
 CAGCTGTAATTTGTGTTGGTGGGGGGGCTGAGGAGAGGGTGGGGGCTGGCTCGCTCCCTC
 CAGCTTCTGCTGCGCTTGCTTGAACATGCGGCCAATCTGGGCACCTCAGGTTGCATCTCC
 ATTCACCAAGATGACCTGTGATGAGGAATCTTCAATAGGATGACAAAGTCAATGCAAAAT
 GTTATATTAACATATACTGGAGTCGTCAAAAGCAAAATBAGAAGAATGACGCTTAG
 AAGTTGCTCATTTAAGCGAGCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAAAAAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRKVLQMQLVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFKFMAYEQIKRLVGSQETLRIHERLVAGSLAGATAQSSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVFNMLGIIPYAGIDLAVYETLKNLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTGAGAAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGCCACAAAAAAG
 CATGCAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAG
 TAAATGCAAGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACTT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAAATTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCCTGGAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAA
 AA

208/330

FIGURE 208

MASLGQILFWSIISIIILAGATAIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEFDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRТАVFADQVIVGNASRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGАНFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

094192.08204

FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCCTCCGCCGGCCTGC
 AGCGGGTTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCACTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACCTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACTGTGTTAGTTCCCTTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGGCCCTTTTCCCATCCTGCCCTTTCTCTGCAGCTGTTTT
 GCTTCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCCCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGC
 AACAGTCTACCCCTTTGAGTGGGCGAACCCTTCCAGCTCTGCTGCCTCCAGGAAGCCCTT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAG
 AGTTTTGTAACTTCAAGTGCTGTTCAAGCTGCGGGGATTTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCATGGACTGCAGAACT
 CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAACCGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGCTCGGA
 GTGGCAGATGCAGGAATGAGCTGTCTATTAGCCTTGCCCTGCCCCACCCATGAGGTAGGCAG
 AATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAAA
 AA

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL
LNQCGSLLYLTLASTDLTAVFICNSLAIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISP EWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

0941992.082801

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAA
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTCACTTCTGTCTGGTGAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTTGAGGTCCTGGGGCTGCACCTTTGCCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTCACTCTGCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLETQVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLLALASLLLRGLLP

09/19/2020 10:26:20

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGCGTTGCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCC**CAT**GTCCCCGCCGCCG
 GC CGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGCGGGGGCCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACAGCAGAGAGCTTCCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCCCTCCCAACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTACAGAAAAACAAAACCTGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLLNIGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTTFFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSVFTMQPIDRNQR

09441992-082804

FIGURE 215

CCCGGGTCGACCCACCGCTCCGGGGAGAAAG**ATG**CCGGCCTGGCGCGCGGTGGTCTGCTAGCTGGGGCA
 GCGGGCTGGCGAGCGGCTCCAGAGCGGACCGTGAGCCGGGTACCGCGACTCGGTACTGCAGTGGGAAGAGCA
 GAACCTGCTCTGGGGCGGCTCTGAATCACTTCGGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGAAGTATGAGTGATGTGGGTACCGCTGGGCTCTACCTCCAGGAAGSTCACAAATGCCT
 CAGTTCCATGGCAAGTGGCCCTCTCCGGTTCCTGTTCTTCAAGAGCCGGCAGCTCGGCCGTGGCCTCTTTTCT
 CAATGCCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGACCTTCGTGCCAGCCTCCTCCCCATGTACCACA
 CCTGTGTGGCTTCGGCTGGGTGTCCCTCAATGCATGGTCTGTGTCCACAGTCTCCACACCCAGGACACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGGCTCAGGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCTTCGGGGCTCTCCTGCTGCTCATGCTGACCGTGACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCTGGTGCCTGTGGAAACAGCGCGCTGCCCTCACGTGCGCAAGTGCGTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTCGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACT**TGA**AGACCTTGGAGCGAGTCTGCCCAAGTGGGGATCCTGCCCC
 GCCCTGCTGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCCTCCACGATCTGGGACTCGAGAGTGGCGAGCCCTCTACCTCCTGGAGCTGAACCTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCGTGTTTCTCCACACAGCCTCCTCCCCACATCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCC
 CTCTGTTTACCACCCCCACCCCTCTCCAGGACACCCTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGGATCTCCCCATGGGATCTTGAGGGACCAAGTGTGGGATTGGGAAGGAGTTTCAACCTTGACC
 GTTGCCCTGACAGGTTCCAGGAGGGCTCACCATACTCCCTTCAGGGCCAGGGCTCCAGCAAGCCACAGGGCA
 AGGATCCGCTGCTGCTGCTGCTGGTGGAGAGCTGCCACCGTGTCTCGGGAGTGTGGGCCAGGCTGAGTGATAGG
 TGACAGGGGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGGCGCATGTGGAGACGGGTGTTGT
 CGSGGAAGAGGTGTGGCTTCAAGCTGTGTGTGTGAGGGGGTGGGTGTGTAGCGTGGGTAGGGGAAGCTGTG
 TCGCGTGTGTTGGTGGCATGTGAGATGAGTGACTGCCGTGAATGTGCCAGCTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCTGTGACCATCAATATCACTGTGGAGCGCCAGCTCTGCCCAAGAGCCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGCCAGGCTGCCGTGTGTGATGTTCCCTCTGTGGTCCCTTTGCCCGCTCTGCCAAAC
 CTCACAGGGTCCCCACACAACAGTGGCTCCAGAGCAGCCCTCGAGGCGAGGAGAGAAATGGGATGGC
 TGGGGCTCTCTCATCTCCTTTCTCCTTGCTTCGATGGCTGGCCTTCCCTCCAAAACCTTCCATTCOCCT
 GCTGCCAGCCCCCTTGGCATAGCCTGATTTTGGGAGGAGGAGGGGCGATTGGAGGAGAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTTCCCTTCCAGAGGGTCTTACTGTTCAGGGTGGCCCCAGGCGAGGGGCC
 AACATATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTTCCCCACAGG
 AATAGAATGGAGGAGCTCCAGAACTTTCCATCCCAAAGGCACTCTCCGTGGTTGAAGCAGACTGATTTTGT
 CTCCTGCCCTGACCCCTTGTCCCTCTTTGAGGAGGGGGAGCTATGCTAGGACTCCAACTCAGGAGCTCGGTG
 GCCTGCGCTAGCTTCTTTGATACTGAAACTTTAAGTGGGAGGTGGCAAGGATGTGCTTAATAAATCAA
 TTCCAAGCCTCAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQP IYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPF SRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFSTVFHTRD TDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPFLFWVLDAHA IWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGTCCGTGA
 CT**ATG**GGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGGCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAA
 ACTCCAATATGAGGACAAGTTCCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCACTGGCAAAATTCAAGGAGGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCATTTGA
 GGAACCTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC
 TTTGATCTTGAATATATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCTCGTGAAGGAGTATGCTGCGT
 TTGTGCTGGGCGCTGCCTTTTCAGCAACCCCAAGGTCAGGTGGAGGCCATCGAAGGGGGA
 GCCTGCAGAAGCTGCTGGTCACTCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
 CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCCTGAAGC
 TCGGGGGGCTGCAGGTCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGTGCTGGCT
 TGGCCATTAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFQGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCG
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGGTTGCCACCCCA
 CGGGGACATCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAAGCCCCCACCCTCC
 TTCCCACTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGGGTTCGGC
 CCGGCTTCGCGCTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTCGGT
 CGCAGGGGCAATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGTGCTGT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTTATTACTTCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAAGCGCAGCC
 TCTTGTAAGGACTGCACTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTACGCCAGTCAGTGACTGGTGGGTTGAATCTGCACTTATCCC
 CACCACCTGGGAGCCCCCTTGTGTGTCCAGGACTCCCCCTGTGTGCTGCTGTCTGCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGATTTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCTCCTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
 AGGCCTGAGGGGGAACCATTTTGGTGTGATAAATACCTAAACTGCCCTTTTTCTTTTTT
 GAGGTGGGGGGAGGAGGAGGTATATTGGAACCTCTTCAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAAGTGGCATTACTGGAACATAATGGTTTAACTC
 CCTTAACACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTCTGTGGTGAAGTGGC
 CACTCCAGAGCTGCAGTCCCATGGAGGAGTCACTACCATGACATCGTAGGGGAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATGGGGTGTGGGAGGGGCGGGAGGTTTTCTATAACTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGAAT
 AATAAAAAAGAAATTTGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGINGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGCTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

0941992-082801

FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

20241992.082604

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTGCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCGGCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACC

FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCNNTCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTCGCGTTTCGGGCCGCGCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTTGACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCATAGTGCCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCCATGGCTACAGCAAGACCCC
 CTTGGATGTGGGTGCTCTGTGCTCTGATCAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTGCGCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTACGGCCGCCCACTGCAG
 GAAGAAAGTTTTACAGTCCGTCTCGGCCACTACTCCCTGTCACCAAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACGAAACAGAGAATTCGTCCCACTAAAGATGTGAGCCCAT
 CAACGCTCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGATCCAGGAAACCATCCAGGCCAATCTCTGAGTCAT
 CCCGAGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTGTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAACGTGCCAGGGCGGGGTTGCGTCTCAATCTCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQFPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQMFQGVKSIPHPGYSHPGHSNDLMLIKLNRIRPTKDVRPINVSSHCPASAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSSGGP
VVCNGLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

094192.02201

FIGURE 227

ATGGTCAACGACCGGTGGAAGCCATGGGCGGCGCTGCCCAACTTGAGGACCGGCGGCGCA
 CAAGCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTCTGTGCCCCGTGGCTGTGC
 TGCTGGCTGTAGCTGTCAACCGTGCCGTGCTCTCTCTGAACACAGCCACCGCCCGGCGGACG
 GCGCCCCACCTGCTGTAGCACTGGGGCTGCCAGCGCCAACAGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCTCTATGACCCGCGCTGCCCGACCTACCGACA
 GCTTTCGACGCTGGAGAGCGCCAGGCGCTCGGTGTCTGCAGGCGCTGCACAGACCAACAGG
 CAGCCACGGTGGTGGGCGACAGGAGCAGGAGCTGCTGGACACGCTGGCCGACAGCTGCC
 CCGGCTGCTGGCCGAGCTCAGAGCTGCAGACGGAGTGATGGGCTGCGGAAGGGCATG
 GCACGCTGGGCCAGGGCTCAGCGCCCTGCAGAGTGAGCAGGGGCCCTCATCCAGCTTCT
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTAGCGACATCTCTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGGGCCCCGCAACAGAGGCCACCTTCAGAGAGCGCCGTGCC
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGCGACGCTTCT
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTCCACCCACTATGCGGCGGCGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGGCGCTGGAGCGGTGTTTACGCGCGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTTACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACACACAGGCTGCCCTACAGACT
 GCACGTGGACCTGGAGGACTTTGAGAATGGCAGCGCCATAGCCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCGTGGACCTGAGGAAGACGGGTACCCGCTACCGCTGGCTGACTATTCC
 GGCACTGCAGCGACTCCCTCTGAAGCAGAGCGCATGAGGTTCACACCAAGACCGTGA
 CAGCGACCACTCAGAGAACAACTGTGCCGCTTCTACCGCGGTGCTGGTGGTACCGCAACT
 GCCACAGCTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCAGCGCTCTATGCCAGCGG
 GTGGAGTGGCTCTGTGACCGGCTGGCAGTACTCACTCAAGTTCCTGAGATGAGATCCG
 GCGGCTCCGGGAGGACCG**TAG**ACTGGTGACCTTGTCTTGGCCCTGCTGTCTGTCCG
 CCACTCCCGCCACCTCACTCTTTCTGTGAATGTTTCCACCCACTGTCTCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGGCGGGGCCATCCCTGACACGAAGCTCCCTGGCGGCTGAAT
 CACACATCGCCTTCTCGCGCTCCCAACCCCTCCATTTGGCAGCTCACTGATCTCTGTCCCT
 TGCTGATGGGGGCTGGCAAACTTGACGACCCCAACTCTGCCCTGCCCGACTGTGACTCCGG
 TGCTGTTTCCGCTCCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGACCCCTGTGCCCTGCC
 GGCCAAATACCCGGCATTAATGGGACAGAGAGCAGGGGGCAGACAGCAACCCAGTATCTCCAG
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTGAGCCCTGAGTCTGAGTCTC
 CCCTCCCAATGCCAACCCCAACCCCGTTTCCTGTGTGCCAGAGACCCCACTCTTCCCCAA
 GGGCTCAGCCTGGCTGTGGGTGGGTGGCCCACTCCTACAGGCCCTGAGGTAGGATGGGG
 GAGCTGCTGCCCTTGGGGACCCACGCTCCAAGGCTGAGACCACTTCCGTGAGGCGCAACCC
 CCTGTGCCCCGGCAGGCTGGGGTCTGCAGTCTCTTACTCTGTGCTCCCACTGCTCTCTGT
 TCTCAAATGAGGCCCCAACCCATGCCCCACCCCTGCAAGGTGGGTGGGGCCCTGCACCTGGGGCT
 CGGGGCTGCCATGCCAATTTCTCTCTGTGGTGGGGCTAGGACGGGCTGGGATGAG
 GGCTGTGCAACCCCAACCAATTTCCAGGCACTCCAGGTGCTCCTAGGAGGCCAACCTTGCC
 GCCTTGGGGGTGATGACCTCTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGCC
 ATTGACCTGGGCACCTGGACCCAGGCTGAGGCGCGGCCCGGCGAGTGGTCAAGGGACAGGCA
 CCACCTACCGGGCAATATGGGTGGGGGAGGCTGCTATCCCACTCTTGTGTGCACACA
 CTTTCTGTGTGAATCTCCCAACTCCAGCAGCTGCATCCCACTCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGAGGCTCCAGGACCAAGGCGAGGCTGGAGCCGCGG
 TCCTCAGCTGTCTGTCTGACGAGCTTGGACCGCTGGCGTACGTGAGGCCAGATGACAGG
 CGGCTTTTTCAGGCTCTGTGAGTGGGGCTCCGAAAGGGCTGGAGTACGCTTGGGGAGCT
 GCCTAGCAGCTTCTGCTGGCAGGAGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GGTGCTAGGGGGTGTGGGTTCCGTTCTCCCTCCCTCCCACTGAAGTTGTGCTTAAAA
 AACAAATAATTGACTTGGCACCTGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCAGTGCCACAGGTCATCCACATGCGCAG

0944092-082801

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELDLADQLPRLLARASELQTECMGLRKGHTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHKSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

094192-0300

FIGURE 229

CGAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAGCTCTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT
 GTCTTCCTTACACTTGGTGGAAATAAGAACTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCTTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAAATACACAAGGAATTTCTTTTGTGTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCCCTCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCGGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCATTTTCTTCCATTGACCCATATTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAATGTAAATACTGTGAAAA

FIGURE 230

MQAKYSSTRDMLDDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDGKAWLWMDGTPFTSELFHIIIDVTSRPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

0941692.082301

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTTCCC

FIGURE 232

CCGGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCGGGG
 CCGGAGCCCTCCGGATCCGCCCCCTCCCGGCTCCCGCCCCCTCGGAGACTCTCTGGCTGCT
 TCGGGGTTTCGCGGGGCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTCGGCCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACCTGAGGCT
 GCTACGCTCACTGGTGGAGAGCCGTGCGGCCAGGCCCGCCCCAACTGGAGACTCTG
 AGCTGCCGCCGCGCGCAACACCAACGCGGCGCGCGGCCAACTCGGTGACGCCGAGCG
 GAGCGCGAGAAGCCCGGGGCCGCGCAAGGCGCGGGGAGAATTTGGAGCCGCGCTTTGCC
 CTACCACTGCACAGCCCGGCCAGGCCGCAAAAAGGCCGTCAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGTTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTCTTCTGAC
 GGGCGCACGGGGCCCGGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCCTGGTGCTGACACCACTACACCGAGGCGCACGGCTGGCACGCCTAAGTG
 CCACCTCAGCTGGCTCCCGGCCACCTGTACCTGGGCCGGCCCCAGGACTTCATCGGG
 GAGAGCCCAACCCCGGCCGCTACTGCCACGAGGCTTTGGGGTGCTGCTGTCGCGCATGCTG
 CTCGAACAACATGGCCCCCACCCTGGAAAGGCTGCCGCAACGCATCGTCACTGGCGCCCTGA
 CGAGTGGCTGGGTTCGCTGCATTCTCGATGCCACGGGGTGGGCTGCACTGGTGACCAGGAG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGACAGGAGGGGGACCTCAT
 TTCCGAAGTGGCCCTGACAGCCACCCTGTGCGTGACCTGTGCACATGTGACAGCTGCACAA
 AGCTTTCCGCCGAGCTGAACCTGGAAACGACAGTACAGGAGATCCAGGATTCAGCTGGGAGA
 TCCAGAATACAGCCATCTGGCCGCTTGATGGGGACCGGGCAGCTGCTTGGCCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCGCATGGCTCACCCGCTGCCCACTGCGTGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCCGCGCTACCAACCGGCCCTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGCCCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCCCGGCCCTCACTC
 GCGGAGTGCAGCTGCTCCGCGCCGTGAGCCGCGTGAGATCTTGCTGTGGCCCTATGCTACT
 GAGGCTCTACGTCTCACTGTGCTGCTGCTCTAGTGGCGCTGAGCGTGACCTGGCCCTGG
 CTTCTTGGAGGCTTTTGCCACTGCACTGAGGCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCGCGCCAGGCCACGCGCTGGCCATGACAGATGCTTTCGCACT
 GTCGAAGGCCACGTGGCAGAGCTGGAGCGGCGTTTCCCGGCTGCCCGGCTGCCATGGCTCAG
 TGTGCAGACAGCCGACCCCTCACCACTGCGCTCATGGATCTACTCTCAAGAAGCACCCG
 TGGACACACTGTTCTGCTGGCCGGGCCAGACAGGTGCTCACGCTGACTTCTGAACCGC
 TGCCGATGATGCACTCTCCGGCTGGCAGGCTTCTTTCCATGCAATTTCCAAGCTTCCA
 CCCAGGTGPGGCCCCACCACAAGGGCTTGGGCCCCAGAGCTGGGCGTGACACTGGCCGCT
 TGTATCGCCAGGCAGCCAGGAGGCTGCTTCTACAACCTCCGACTACGTGGCAGCCCGTGGG
 CGCTGCGGCGAGGCTCAGAACAGAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTCTCTCACTTCTCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGACGAGCT
 ACCGGGCCAGAGCTGACGCGGAGGCTCAGTGAGGACCTGACACCGCTGCTGACGAGC
 GTGCTTGAGGGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTTCTTGAACAGGAGAGGG
 CAACAGCACCT**TGAC**CCCCACCTGTCCCGCTGGGCGTGCCGCTGGCCGTAGCCAGACCCC
 CTCCCCCAAAACAGAGCCACTGCGCAGCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCCC
 AAGCTGGGCCACTGGTCCCCCTCTCGGCTCTGTGGTCCCTGGGCTGTCGACAGACTGGG
 GGAGCTGCCCCAGAGCCACCACTTCTCATCCCAACCCAGTTTCCCTGCCCTGTAGCGCT
 GCTGATTGCGGCTGTGGCCCTCCACGTATTTATGCAGTACAGTCTGCCTGACGCCAGCCCTGC
 CTCCTGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCCACTTCTCCCTTTTGACCTGCCGAAGCTCCCTGCCCTTAAATAAAGTCGCCCA
 AGTGTGAAAAA

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPRGNTNAARRP
 NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQLRLVAVL
 TSQTTLPTLGAVNVRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
 QHGDDFDWFPLVPDTTYTEAHGLARLTGHLSSLASAAHYLGRPDPIGGEPTPGRYCHGGFG
 VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGE
 VQEGDPHFHSALTAPHVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
 AAWPVGIPAPSRPASRFEVLRWDFYTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
 RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
 LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
 HADVFAVPKHAHAELERRFPGARVPWLSVQTAAAPSLRLMDLLSKKHFLDTLFLLAGPDTVL
 TPDFLNRCRMHAISGWQAFPMHFQAFHPGVAAPPQGPPELGRDTRGRDFRQAASEACFYNS
 DYVAARGRLAAASEEELLESLDVLEVLFHFSHLHLVLRVAPEALLQRYRAQTCARSLEDL
 YHRCIQLSVLEGLGSRTQLAMLLFEQEQQNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAAGTTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTTCCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAAGTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAAAAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTCT
 TTCCCCGCCCTGAGACCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGAGCGGCGACGCGAGGGCTCCCGCCGCCCGCTCCGTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAAGTGTATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGCTCTCTT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACCTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTAATAACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAAGTCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

235/330

FIGURE 235

MAAGLFGLSARLLAAAAATRGLEAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

108280-2664660

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACCCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGCTTTCGACCCAGCA
AGATCCAG

0941992-082804

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAAACCCACGCGACAGCCTGCGGGAGGAACTTGTATCACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGAGGACCCGATACCTGGGGGCCACCCCTTCTGTC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGA
 TCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
 CCCTGGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCTCTGGGAGCTGAGGCAGACCTGTCAAGTTGTATTGTATGCCTTC
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 CAGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCTATCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGGAAGAGACCCAGAGAAATGAGGCCCCCAGTGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCCACTCTCTGGAGATGCTGATTACAGTGCCG
 GCCAATCAGTCAACAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTGCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCTCACCCGAACCTTCCACATCAGGAGCCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGCGCGCCGAGGTGTCCCCCACTCT**TGA**TT
 TCTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAAGTGCCTGGACCAGGTCAAGGC
 CTACAGCTGTGTTGCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTTGAATTA
 CTTAGAAATTCATTCTCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATTAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCATCACCACAGAAAGGTC
 GGCTGGCAGACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGGA
 TGGAGTTTACTGTTTGTGGAATAAAACCGGTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPAKALGQLISKYSRLRELHLSFTQGFWRTRYWGPFPLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVPTASFKEPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSI SWELRQTLSVVFDAFITG
QGKKDWSLFRMFSTRLTEPCPLASESRVYVDITTYNQDNETLEVHPPTTTYQDVILGTRKT
YAIYDLDDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLDDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLNLPTPDFSMPYNVICLTCTVVAVCYGSFYNNLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

03941992.082804

FIGURE 239

CAAC**ATG**GGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAA**TGAT**GTGCTGGGTCCTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCACTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCFADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19 '

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACCTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACC**ATG**AGGTCCCTGGCTGTGGAGATGCAGGCACCTGAGCCAAGG
 CGTCCAGTGGTCCCTTGGCTTCTGGCTGTCTGGTCTTCTTCTCTTCGCCTTGGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCAGGAGGACAAACCTCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGGCCCAAGGCCCAACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTTCCCAAAGTCA
 GCACAGAATGCTGGCTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCTATCCCACTTAAGGAGAAGAAACCTCAGGCCACCCCAACCCCTTGGCCCTTTCAG
 AGCCCGACGACGACAGAAACCAAGACTGAAGGCCGCCAATCTCAAAATCTGAGCTCCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAATAGGAGGCCCTCAGACGACTTGGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTGCCTGTGGCTCCAGAAACTCTTCTGCCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC
 CTTTGGCTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGACCTCCGGTGCTCACTCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACGCCTTCTCCCTGACCAAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCCGTACTTGCACCTTCTGGAAGGCAC
 CCGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAGACTCTT
 TCTGGTTACGGCACAGACCCCGAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACAGCGCTCCTGGTC
 CCGGAAGTCCCAAAGCCAAAGAACT**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTGGCAATTCAGCTGGCTCGAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATTGCTCAATTGAGGTTCTGAACTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCAACAATTCTGCTGAAGAAACACTCTT
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC
 AGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATTTAGAAGGGTCTATAGTCTGTCTGTG
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACCTGATAATATACAAATGATTTGT
 GTCCATGGAAAGGCAATAAATTTTCTACAGTGAAAAAAGAAAAA

094192-062601

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSFRGQDAGMASGRTEASWKSQDQTKTTQGNNGQTRKLTASRTVSEKHQ
 KAATTAKTLIPKSHRMLAPTGAIVSTRTRQKGVITAVIPPKEKKPQATPPAPFQSPTTORN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLENLTFLDSRHF
 NQSEWDRLEHFAPPPGFMELNYSLVQKVVRFPFVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHDPDFL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFS DHYYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPFGGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGAATGCGCGGACCGGGCACCCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAATCTATCTTTATACATCCCTCATGG
ACAAGAGATTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

244/330

FIGURE 244

MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

2025.05.04.16.0

GGGCTGGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGCTCTGCGGTCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACCAATGCCACCCGCGGGGCTCCGCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTGGTGCTGGGGGCTCCCCGGTGCTGGCCGGCAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCTGGCATCCGGGGTTAACTGCGAGTTCTTACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGTCTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCTTGTTCCTGTTGTACTCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCTGCGAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACACGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGAGGCTGAACATAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAATAGTCCCTCTGCTCCCAAGATCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCTCCTCTGTTGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTGACGAGCTGGCAGTAGGCCCTCCTCTGCTGGCTGGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQFPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPFPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCAAGGGTGAGGGCGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAAGATGGTGTCTTCTGCCCTCAAATGGTCCCTTGAACCATG
 TCATTTTCTACTTTCTCACTGTTGGCTCTCTTAACCTGTCCACTCTTCATGGTGTCAGAG
 CACTGAAGCATCTCCAAACGTTAGTGATGGGACCACTTTCCCTTGAATAAAATACGATCTC
 CTGAGTAGCTCATCCAGTTTCATTATGATCTCTTGATCCATGCAAACTTTACCAACGCTGACC
 TTCTGGGGAAACACGAAAGTAGAAATCACAGCCAGTCAAGCCACCAAGACCATCATCTGCA
 TAGTCAACCACTGAGATATCTAGGGCCACCCCTCAGGAGGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTTGCAGGTCTGGAAACACCCCTCAGGAGCAAAATGTCACGTCTGGCTCCCGAG
 CCCCCTCTTGTGGGGCTCCCGTACACAGTTGTCATTCCTATCTGCTGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAGGAAAGGGAACCTGAGGATACTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATTAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGACGAAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTCTAGAATTTTATGAGGATTAATTCAGCATACCGTATCCCC
 TACCCAAACAAAGATCTTGCTGCTATTCGCCGATTTTGAAGTCTGGTGCATGGAAAACCTGGGA
 CTGCAACATATAGAGAATCTGCTCTGTGTTTGAAGTCTGGTGCATGGAAAACCTGGGA
 GCTTGGCATCAAGTGCATGTGCGCCATGAATGGCCACCACTGGTGGGAAAACCTGGTCA
 CTATGAATGGTGAATGATCTTTGGTCAATGAAGGATTTGCCAATTTATGGAGTTTGTG
 TCTGTCAAGTGTGACCCATCTGAACTGAAAGTTGCAGATTATTTCTTGGCAAAATGTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTCTTACACCTGTGGAAAATCCCTG
 CTCAGATCCGGGAGATGTTTGAATGATGTTCTTATGATAAGGGAGCTTGATTTGAAATATG
 CTAAGGGGATATCTTAGCGTGCAGCGATTTAAAGTGGTATTTGACAGTATCTCCAGAGCA
 TAGCTATAAAAAACAAAAACGAGGACCTCTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATCTCATCTCATCTCAAT
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACATGCAGAGGGGTTT
 TCCCTAATAAACCATCACAGTGAAGGCGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AAGGCTCTCAGCGGCCGCCCGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATACC
 AGCAATCCCAAGCATGGTCCATCGATTTTGTGTAACAAAAACAAAAACAGATGTGCTCATCTCCC
 AGAAGAGGTGGGAATGGAATGGAATTTAATGTGGCATGAATGGCTATTACATTTGCAATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAAGCAT
 AATGATCCGGCAAGTCTCATTAAACAATGCATTCAGCTCTGCAGCATTTGGGAAGCTGTCCAT
 TGAAAAGGCCTTGGATTTATCCCTGTACTTGAACATGAACCTGAAATATGTCGCGTGTCTT
 AAGGTTGAATGAGCTGATTCCTATGATAAGTTAATGGAGAAAAGAGATATGAATGAAGT
 GAACCTCAATCAAGCCCTTCCTCATCAGGCTGCTAAGGACCTCATTGATAAGAGACATG
 GACAGCAGAGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACCTACTCTCCGCGCTGTG
 TGCACAACATCAAGCCGTGGGTACAGAGGGCAGAAGGCTATTTGAGAAGTGGGAAGGAATCC
 AATGGAACCTTGAGCCTGCCCTGTCGAGTGAACCTTGGCAGTGTCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTATAGTAAATATCAGTTTCTTTGTCCAGTACTGAGAAAA
 GCCAAATGAAATTTGCCCTGCGCAACCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCCACAAATTTCTTACACTCATTTG
 CAGGAACCCAGTAGGATACCACTGGCCTGGCAATTTCTGAGGAAAACCTGGAACAAATGTG
 TACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCACATGGTGAATGGGTACAAACAAATCAA
 TTTCTCCACAGAACACGGCTTGAAGAGGTAAGAGGATTTCTGAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTTGTGTCACACAGACAATGAAACCATGGAAGAAAACATCGGTTGGATGG
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAGTGAAGTGAACGATTTGAAGTATGTA
 TTCTCCCTTCTGCCGCTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTGGCTCCAACTGGGAGATCTTTTTCCCTTCACTGATTTTTTGA
 CTATCCCTGTGAAAAGAAAGCTGTTAGTTTTTTCATGAATGGGCTTTTCACTGAATGGGCTA
 TCGTACCATGTGTTTGTGTTTCATCACAGTGTGGCTGCAACGTAACCCAGAGTGTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETHFGFYKSTYRTKEGELRILASTQFEPTA
ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVABGLIEDHFDVTVKMSITYLVA
FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFISIPYPLPKQLDAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFNGNLVMTMEWNDL
WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGD
FCSRSQHSSSSSHWHQEGVDVKTMMTWTWLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
TGYLWHVPLTFITSSKNMVHRFLFKTKTDVILPEEVEWIKFNVGMNGYYIVHYEDDGDWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLEKMRDMNEVETQKFAFLIRLLRDLIDKQWTDEGSVSEQMLRSELLSLSTACVHNYQPCV
QRAEGYFRWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFLLSLSTEKSQIEFALC
RTQNEKELQWLLDESFGKDGIKTQEPFQIILTLIGRNPVGYPPLAWQFLRKNWNKLQVQKFELGS
SIAHMMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTITETLEENIGWMDKNFDKIR
VWLOSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGGCACAGACGGGT**ATG**AGCGCGGTATTACTGTCTGGCCCTCCTGGGGTTCATCCTCCCA
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCGCGCTACTGAGACCCGGATGGGCCCCGGGCTCTCCCTGAT
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCTCCTCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGACTGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTTGGGCCGTGGGTATGACTGAGA
ACTGCAATAGAGAAAGATTTTCTGACCTGTATCGGGGAGCCACATTATGACACACGGAAAC
TTGGTCTCAAGAACCCACTGATTGGACCATCGAATACCAGATGTGCGAGGTGGGGCAGGT
GTGCTCAGGAGACCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAA
GTGTCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCT
CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACCACACCAGACAAATCG
GGATCTTCTCTGCGCTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCTTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCCTTCTGTG**TAA**CTCTATTACCCCCACGATTCTTCCACCGTGCTGA
CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACAGATTCTTTTC
CCATTCTGTCCATGAATCACTTCCCCACACAACTATTCATCTACTCACTTAACAGCA
ACACTGGGAGAGCCTGGAGCATCCGCACTTGCCCTATGGGAGAGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCHYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGVQCQETL
LLIDVGLTSTLVGTGKCSSTVGAQNSKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLN
SLPPQAAFPVPGDRQCPTCVQPLGTCSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSFLNHNTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWGWVVC
PSC

FIGURE 251

GCAGCAGGGCAGGACGCCCGCTTCGCTAGCGCTGCTCAGGAGTTGGTGTCTGCCTGCCTGCGCT
CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTCTGCTACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGCGCCCCGACGGCCTGGAAGAGTCT
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGCAGTGTGGGTGCTCAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGTGACATAGGACCCCC
TGGTCTAATGGAGAACCAAGGCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTTCATCAAGAATGCTGTGCGC
GGTGTGCGCGAGACGGAGAGCAAGATCTACTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCAGCTGTCTGCCAGGGCCGCGGGGACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATC**TGA**GCCTCAGGCTGGGGCTGCCATTGGGGCCCCACATGTCCCTCGAGGGTT
GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGCCCTGTGTAAGGGTGGAG
GCTCACTGAGTAGGGGTGTGTGTCTAAACTGAGAAATGGCCATGCTTTAAGAGGAAAAATG
AAAGTGTCTAGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCAATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

252/330

FIGURE 252

MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRFPGRVG
PTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKF IKNVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

090109Z-082001

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSFEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGCTGTGCTGGACGCGGGAGACCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTGTGCCCCAGGAGCCAGGCTGCCCGCTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTGGGTGGTGTATCCCCCTTGGGGC
 TGCTGTTCTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG
 GGCTCAGCAAAATACAGCACAAAGCTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCAGGGGGTGGGGC
 CTGGGCCACAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGCTTGAATCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACTTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGGAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACTTCCTTCCTGGCTGGTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAACATGGTAAGCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCCTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCAAAA

FIGURE 256

MSCVLGGV I P L G L L F L V C G S Q G Y L L P N V T L L E E L L S K Y Q H N E S H S R V R R A I P R E D K E E I L M L
H N K L R G Q V Q P Q A S N M E Y M V S A G S G R R G W H R G W G L G H Q P A L F P S Q L C S P A S A C D G W L R V S S G R
G G S R L C S V L F V C F E T G S H S A T D A G V Q W H N R H A L K P

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**TAT**GGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTT
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAAATAAAATTCGGTATGCTG

0947168-0

FIGURE 259

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAAATAGAAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAAGCTTCATTCAGTGTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTACGCTA
GTAAATAGAAACCTGTGTTTATTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTGAAATTTACAGTACTGCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 261

GAGGATTGGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAAGAGACTGCCCTGCTTGGTGTGTTTGCAGG**ATGAT**GGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTCTCTGTTCCCTGCAGCTTTTCTGCCCCCGCCGAGTGAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACGAGGGCATACATCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCACCTGAGAGTTGAACGTGCCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACCAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCAGCAATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGATACCCCATGCAAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGCCA
 GGGCCCTCATCGCATCACTGTCATCTATGATCCACTGGGCACATCATGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACACCCAGAGAT
 AAGCAGCTCTATGCCGTGGAATGAAGGAAACAGATCATTTACAACTCCAGACAAAGAGAAA
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCTTTCACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTCCTTTCCCAATGTCACTGCGCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT
 GCTCCCCAGCATTTACTGTAACCTGCCATCTTCCCTCCCACAAATTAGAGTTGTATGCCAGC
 CCTAATATTCACCACTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCCAACTAAAATACTATTAATATTTCTTT
 CTTTCTTTTCTTTTTTTTGGACAAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCTGGCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAATACATATTTCTTATTGAGGTTTAACTCTATTTCCTCCCTAGGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAGTGAAATATTAAACATTTACATATCGCTTT
 CCAGGTGTGGAGTGTGTCACATCATTGAATTTCTCGTTTACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTACAAGTGAAGATACAGC
 TAGAAAATACTACAAATCCCATAGTTTTCATTTGCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATATAGTCTGTCCC
 TTTAGCCGATTTTCACTGTCTGCAACAAGACCTTCAATAGGCCTTCAAATGATAATTCCCTCC
 AGAAACCAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTGTCTGTCTGTCTGTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVVALRGASALLVFLAAFLPPFQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRQCTYTSEYKSAVGNLALRVERAQRIDYIQYLRADCEIVSEDKTLAEMLL
QEAEEEKIKIRTLNLASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPA PRKQILTLWSWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSFSTYIDLAVDEHGLWAIHSGPGTHSHLVLTIKIEPTGLVQHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGHPRITCIYDPLGTISEEDLNLFFPKRPRSHSMIH
YNPRDKQLYAWNNEGNOIYIKLQTKRKLPLK

FIGURE 263

GGGCGCCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTCCGGAGTTCATGGGGCTGTCGGTGTTCCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGGCCGCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAGAAGCAGAAAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCTTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACTGGAGCTGGACCACGCCACCCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGCTTGGCTGGCCAACGGGGACACCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAGGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCCTCGTGTGGCTTACCCACAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCCTTCGAA
 CTAAGGGGCACTCCGCGGCTGTGCATCTGTTGCTTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTTGCTGAAGACAGGCCGCTTTGAAGAGGCGCGGGTGCCCGCGCGGTGCCGC
 CTGGCCCTCTCCCCAACGCCACAGGCTTGGCCTTGGCCAGTGGCAGTAGTATTCACTCTTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCCAGTGTATCGCCA
 ACTTGTCTTTGACATCAC'TGGCCGCTTTCTGGCCTCTGTGGGACCGGGCGCTGCGGCCTG
 TTTCAACACCTCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTGA
 AGAGCTTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGGCCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTCTGGCTGTGACTCCTCCTGACTAGTGGCCAAAGTGCTTTTCTTC
 CTCCAGGCCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAATGTGATTTTGGCCTTGTGGCAGCACATCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAAGCTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCCTCAGTTCTATTGTAAGATGGAGAATAATCTCTCTGTGAACCTCCTTGGA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAGACT
 AGTACTATTGTCTCAATGTCTATGAAAGTGGTAAAGTGGGAACAGTGTGCTTTGAAAACCAA
 TTAGAAACACATTCCTTGGGAAGGCAAGTTTTCTGGGACTTGATCATACATTTTATATGCT
 TGGGACTTCTCTCTTCGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTTCATCAAG
 TTCATCAGATATTGAGTGGCCACTCTGTGCCCAATAAATATGACTGGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFFPDKSSGSKKQK
 QYQIRIRKEKPQQHNFTHRLLAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
 REHRSMRANVELDHATLVRFS PDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDEFKK
 HKAPVIDIGIANTGKFIMTASD TTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
 FTPDVKVWEVCFGKKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWD TDV
 EYKKKQDPYLLKTGRFEEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
 GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQRLQQQLTQ
 AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGGCACAAGGTCCTCTCTCAGGAAACGCA
AGCACCAACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGCTCCATGGACTGAAGAACATCAATTTT**TAG**CGCTTGCCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGTCTAGTAGCACAATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGGAG
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTTCCCTCCCTCCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG
CCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCCCTCAGGCCCTTACGTGAGGTCTGTGAG
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAAGTCAGCCTGTGGCTGTGGCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCCTCTGAGGCCCTCTTACCACACTTTACAGT
TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAATAAGTCAATAGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGCAATTAGGTTGTTTCTTAAACAACCTCTTTCCA
AGGATCAGCCCTGAGAGCAGGTGTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
TGGGAGCAAGGGCAGGGGACAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAGCACCAACTGAAAAA

266/330

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHP
GSHKVPFFRRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

2025.06.16

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAGGGGAGGCACTTGAGAA**ATG**TCTTTT
 CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAACACTGGAGAAGGAACCAAGGACTTTCAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTTAT
 FTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAA**TGAT**
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTTACTCTCAGTATGGATT
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACCTTGAGGTCTGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACITGAACCTGGGAGGTGGAGGTGCGGTGAGCTGAGATCA
 CACCACTGTATTCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKLTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWVYNFFRAWNGGFSGNLEGEFILGGVFV
VSGGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

0901002.002001

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACAGGAACCTGAGCTAGGTCAAAGACGCCCC
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCCACCCAGCCC**CATG**GC GAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCTTG
CTCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAAGGGCTGCCTGCCCATC**TAGG**TCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACACAGGCAAGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTCTAAATTGGACT
TTATTAATTTTAAATCAGTAACTGATTTTACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

09041992.082001
100380.267760

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTATTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCCTGCTGCACCAAGTCAAAATACTTCTTCATTAAAGCTGAATAATAATGGCTTTGAAGATA
 TTGTTCATTGTTATAGATCTCTAGTGTGCCAGAGATGAAAAATAATTTGAACAAATAGAGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTCTTTTTCAAAA
 TGTATCTATATTAATTCTCTGAGAAATTGGAAGGAAAAATCTCAGTACCAAGGCCAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGACCCACCTACACTCCCGAGTAGATGAACCA
 TACACCAAGCAGTTACAGAAATGTGGAGAGAAAGGCCAATACATTCACCTCCACCTGACCT
 TCTACTTGGAAAAACAATAATGAATATGGACCACCAAGCAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCTGCTAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGAGGTATCTCTGGTAGAAAAAGAGCTTTTATAA
 GTGTCAAGGAGGCAGCTGCTTAGTAGAGCATGCAAGATTGATTCTACACAAACCTGTATG
 GAAAAGATTGTCAATTCTTTCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTTATG
 CAAAGTATTGATTCGTGTGTTGAATTTTGTAAACAAAAAACCATATCAAGAAGCTCCAAG
 CCTACAAAAACATAAAGTGCAATTTTGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTAaaaaacacataccatccatggtagacaccacctctccacctgtctctcattgctgaagatc
 agtcaaaagaattgtgtgcttattgttcttgataaagctggaagcatggggggaaggaccgct
 aaatccgaatgaatcaagcagcaaaacattttctcgtgcagactgttgaataatgcatccggg
 tggggatggttcactttgatagtagtgcacatttgaataaagctattcaaaaataaaagc
 agtgatgaagaagaacacacactcattggcaggatttacctacatatcctctgggaggaactccat
 ctgctcttggaaatttaaatatgcatttcagggtgattggagagctacattctcaactccatggat
 ccgaagtagctgctgtagctgattggggaggataaacactgcaagttctctgattgatgaagtg
 aaacaaagtggggcccattgtttcattttattgcttttgggaagagctgctgatgaagcagatgaat
 agagatgagcaagataaacagggaggaaagtcatttttatgtttcagatgaactcagacagagtg
 gccctcattgtagctttttggggctcttacatcaggaataatctgactctctccagaagtccctt
 cagctcgaagagtgaagggattaaactgaatagtaattgcctggatgaacgacactgtcataat
 tgatagtagacgtgggaagagacagcttcttctcattcactgaacactctgacctccagta
 tttctctctgggattcccagtggaacaataatggaataattcacagtgatgcaacttccaaa
 atggcctatctcagtatccaggaactcgaaggtgggacttgggcatcaacttctcaagc
 caaagcgaaaccagaaacatttaactattacagtaacttctcagcagcaaaattctctgtgct
 ctccaattcacagtgaaatgcttaaatgaataagcagctaaacagtttccccagcccaatgatt
 gtttagcgagaattctacagaagatatgtacctgttcttgagccaattgtgactgctttcat
 tgaatcacagaattggacatacagaagttttggaacttttgagataatggtgcaggcgctgatt
 ctttcaagaattgatggagcttactccaggtattttacagcatatcacagaaattggcagatat
 agctttaaaggtcgggctcatggaggagcaaacactgccaggctaaaaattacggcctccact
 gaatagagccgctacataccagcctgggtagtgaacggggaattgaagcaaaccccgcaa
 gacctgaatttgatagaggaactacagacccttggaggatttcagcgcgaacagcatccgga
 ggtgcatttggatcacagaattgccacagttcatgaggataagattattctacatggcagcaccag
 gagataattttgatgttggaaagttcaacgttatatcataagaataagtgcaagattttctt
 catctaaagacagttttgatgatgctcttcaagtaataactactgattctgtcaccaaaagga
 ggccaaactccaaggaagctttgcatttaaaccagaaaattctcagaagaaaattgcaaaccc
 acatatattttatggcatttaaaagtagataaaagcaatttgacatcaaaagattccaacatt
 gcacaagtaactttgtttatccctcaagcaaatcctgatgacattgatcctacacactgcc
 tactcctactcctactcctgataaaagtataattctggagtttaattttctacgtgggtat
 tgtctgtgattgggtctgttgttaattgttaactttatttttaagtaccacatt**TGA**acattta
 acgaagaaaaaaattcttcaagtagacctagaagagagtttttaaaaaacaaaacaaattgaagt
 aaagatatattttcgaatttttaaaattcatcccatgtgtgatcatataaaactcataaaaaattt
 ttaagatgtcggaaaaagatactttgatttaaaataaaacactcatggatattgtaaaacattgt
 caagattaaaaatttaagttttcattttatttttttttttttttttttttttttttttttttttt
 aaagattcctttttctactgatactcgttgatttaatttttttttttttttttttttttttttttt
 gatatttccaaattgcatacagaaataaaatcatctatctgagtagtcaaaatgacagataaa
 cgagagcaataaaacaacattttggaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
 aa

0941992.082601

MGLFRG FVFLVLCLLHQNS TSFIKLNNNGFEDIVIVIDPSVPEDEKII EQIEDMVT TASTY
LFEATEKRFF FKNVSILIPENWKENPQYKRPKHENH KHADVI VAPPTLPGRDEPYTKQFTEC
GEKGEYIHTFPDLLLGKKQNEYGPPGKLFVHEWAHLR GWFDEYNEDQP FYRAKSKKIEATR
CSAGISGRNRVYKQGGGSLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVINS SEDFKNTIPMVTPPPPVFVSLLKISQRIVCLV
LDKSGSGMGKDRLNRMNQAAKHFLLTQTVENGSSWVG MVHFDSTATIVNKLIQIKSSDERNTLM
AGLPPTYPLGGTSCSGIKYAFQVIGELHSQLD GSEVLLITDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDP SGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTTITVTSRAANS SVPPITVNAKMKNKDVNSPFSPMIVYAEILQG
YVPVLGANVTA FIESQNGHTEVLELLDNGAGSD FPKNDGVYSRYFTAYTENG RYSLKVRAGH
GANTARLKLRP LNRAAYIPGWVWNGEIEANPRPEIEDTQRTLEDFSRTASGGAFVVSQV
PSLPLPDQYPPSQITDLDTAVHEDIILTWTAPGDN DVGKVGQRYIIRISASILDLRDSFDD
ALQVNTTDLSPKEANSKSF AFKPENISEENATHIFIAIKSIDKSNLTSKVS NIAQVTLTFIP
QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAGACCGGGAAAGACCATACGTCCCCG
 GGCAGGGGTGACAAACAGGTGTCATCTTTTGTGCTGTGGCTGCTCTTATTTCAAGGAAAG
 ACGCCAAAGTAAATTTGACCCAGAGGAGCAATGATGTAGCCACCTTCTTAACCTTCCCTCTTGAACC
 CTCCTTAGGTGAGGAGCAACTTTGTGGGCTGCGTTCTTAGAGTGTCTGAGAAGTGACTTGCCTGA
 GGGTGAGCCAGAGAAAGGAAGGTGCCCTTGTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGGTGAAAACTTGGAGATTTCACTTCAGTCATTGCTTGTGCTGCAAGATCATCTTTTAAAA
 GTAGAGAAGCTGCTGTGTGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGAAATGGATG
 CAAGCAGCTCCGGGGGCCCAACGCATGCTTCCGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGG
 GCCCCGGCTTTAGGGGATGCCACCGGTTCTGGACGATGGCTGATTCTGATGATGATGTTCCGCC
 GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCTCTCTGCTGTGCTATCTGTG
 CCTGTACATGTTGGCTGCACCCCAAAAGGTGACAGGAGCAGCTGGCAGCTGCCCGGGGCCAACAG
 CCCACGGGGAAGGAGGGGTACACGGCCGTCCTCAGGAGTGGGAGGACGACGCCCACTTCTGGA
 CGAGCCTGAAGCGGACGATGCCACAGCTCAAGGAGGAGCTGCAGGAGGAGCTGACAGCTTCAGGAA
 TGGGCGATACCAAGCCAGCATGCTGCTGGCTGGCTGTGACAGGAGCCCCAGAGAAACCCAG
 GCGGACCTCTGGGCTTCTGTCAGCTGCGAGTGGGACAGGAGAGTGAAGCTGCGCTCAAGCTGG
 CACAGAGTAGTACAGCAGTGCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
 CTTTACCCGCCCCCGGAGGAAGCCTGTGAGGAAGGACAAAGCGGATGATGTTGGTGAAGCCATT
 GAATCAGCCTTGGAGACCTGAAACATCTGCAGAGAACAGCCCCAATCACCGCTCTTACACGGCCT
 CTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGACAAAGGCAATTGATGAGCTCACCTTCAA
 AGGGGACCACAACACGAATTCACACGGCTCATCTTATTTGACACCTGACGCCCATGAAAGTG
 AAAAAATGAAAGCTCAACATGGCCACACGCTTATCAATGTTATCTGTCGCTTACGAAAAAGGTTG
 ACAAGTCTCGGGCAGTTCATGCAAGATTTTCAAGGAGATGTGCAATGAGCAGGATGGGAGAGTCCATCT
 CACTGTTGTTTACTTTGGGAAAGAAATAAATGAAGTCAAAGGAATCTGAAACACCTTCCAAA
 GCTGCCAAGCTTCAGGAAGTTTACCTTCATCCAGCTGAATGGAGAAATTTCTCGGGGAAGGAGCTTG
 ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAAGCTGCTCTCTCTTTCTGTGATGTGACATCTACT
 CACATCTGAATTCCTCAATAGCTGTAGGCTGAATACACAGCCAGGAGGAAGAGCTTTTATCCGATT
 CTTTTCAGTCAGTACAATCTGGCATAAATACGCGCACTTGGATTGGGATGAGCTGTGATATCG
 AGCTGGTCTATAAGAGCAAGAACTGATTTTGGAGAGACTTGGATTGGGATGAGCTGTGATATCG
 CTCAGACTCTCATCAATATAGTGGCTTTGATCTGGACATCAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACGCAACCTCATAGTGGTACGAGCGCTTGGTGGAGGACTCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGTCATCAGTCCAA
 GGCCATGAACCGAGCATCCACGGCCAGCTGGGCTGCTGGTGTTCAGGCACGATAGAGGCTCAC
 CTTGCAAAACAGAAACAGAACCAAGTAGCAAAAAACA**TGA**ACTCCCAAGAGAAGGATTTGTGGGAGA
 CACTTTTTCTTCTTCTTTGCAATTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGAGC
 ACAAAAGAAATGGAGTCAATGGGTGAGAGATGAGAAAGCCCTCGGATTTCTCTGTTGGGCTTTTTAC
 AACAGAAATCAAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTGCAACCTGTGAAGTGTGAC
 AAGGCAGATGCTTTTGAGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTGATAAATCACT
 GAGACCTGTTGTTTGTGTGCTCATTCGAATATCATGATTTAAGAGCAGTTTGTAAAAATTCAT
 TAGCATGAAAGGCAAGCATATTTCTCTCATATGATGATTTAAGAGCAGTTTGTAAAGTGTCTAGG
 AATGCTAAATATCAGAGGAGGAGGAGGATAGGCTTATATGATCATAGTGGACATTAAGTA
 AAATAAATGGACCAAGAAAGAAAGAAACCAATAAATCTGTTGTCATATTTCCCAAGATTAACCA
 AACTATCTGCTTATCTTTTGGTTGCTCTTTAACTGTCTCCGTTTTTCTTTTATTTAAAAAT
 GAGCTTTTTTCCCTGTGAGTTATAGTCTGCTTATTTAAATACCACTTTCGAAGCCTTACAAGAGA
 GCACAAAGTGGGCTCAATTTTTATTTTTTAAAGAGATACTTTGAGATGCAATATGAGAAGCTTTCA
 GTCAAAGCATCAATTTGATGGCCATATCCAAGCATGCCAATGCTGATCTGTCAGGCATGAAT
 GTCAGGCATTGAGACATGAGGAAGGAATGTTTGTACTAATACAGACGTACAGATACTTTCTCTGAA
 GAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAGAAATGACACTTTCTCTTACAGAA
 AAGGAACCTCATTCAGACGTGGTGATATCGTGATGACCTAAAAGTCAGAAACACACTTTCTCTCA
 GAAGTAGGGACCGCTTTCTTACCTGTTTTAAATAAACCAAGATATCCGTTTCTCTTACAGAA
 TATATATATATGTAAGAGTAAATCTGCTGCTTCTCAAGAAATGAGCAATGAGCAAAATATATAT
 CCAAGATGCTTCTGAAATTCGATTTTTATTACCATTTTCAAACTATTTTTTAAAAATTAATACAGTA
 ACATAGAGTGGTTTCTTTCATTCTATGTGAAATTTATAGCCAGCAGCAGATGATGAGCTAATATCT
 CTTTGGTGTGTTAAAAATGCAATGTGATTTGATTTGATTTGATTTTATGAATTTTAAATAAACAC
 AGGCCATGAATGAAGGTGGTATTGACAGCTAATAAATATGATTTTGTGGATATGA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLVELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAANTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDDIKGWGGEDVHLYRKYLHSLNLIIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

090499-00001
100230-266406

FIGURE 277

GAAAGAA**atg**TTGTGGCTGCTCTTTTCTGGTGACTGCCATTTCATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTCTAAATGACCAAACT
 CTGGAATTTTAAAAATCCCTTCCACACTTGCAACCACCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGTTGTGATATTTGTCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCA**tga**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCGCTTCCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACGAC
 TCAAAATATTTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTTGTGACCATTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

0994992-032301

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCACTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCAA
 GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATTCAAACTGTTAAATGACATTTTATTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTCTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIQEIRLSVVHTVRFSEIHFLALAIGSACALMIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEEERLNQEKVSVYLETD

09041992.082504

FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAATATTCATGCTTCCTGTGATTTC
ATCCAACACTTACCTTGCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAA

282/330

FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

094193-00004

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTGTCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**AATG**C
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTGTGTCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAAA**ACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA**AA**ACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAAATGGTGAACCTTGTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
 GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCGCTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

094391-05204

284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRIQPFVTERTLGKVQRWSGVHTQTGGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWFPVGVARGGALCQ

0941992-082801

GT**CATG**CCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
GACCTTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTCGGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAAC TGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGAGGAGGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGCAGGACAGACAG
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAGGCATGTA
CCCTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

286/330

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRGTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

00941992-108801

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAGGCCAGGA
 AGCACAGCAAA**AC**GTGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTTACAAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGCAAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAA**ACT**GTGTCTGTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGCAGCAGCAAGAGATACATATGCGAGTTACCATCCC
 TAA**ATAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTCAATGA
 TCCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCGTCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTCAAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTCAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGCTCT
 GCCATATCAGAAACACAAACCCCTGAAGAGTTCTGATTGTGATTTTCTTTTCTTCATGCC
 TACCCCTTTTTTGGAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACTTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAA**ACT**GAATTTAAAGAAATGCTATCTTGGA**AAAT**GCATACGTCTGTGCAATT
 TTTTATCTGCCTAGTGCTATTCTGCTGTGTTAACTAGATTGTACAAATAACTTCAATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAAGCAAA**CAAT**TTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT
 CCCACTTTGCAAACTTAACTACACATGCTTGAATTAAGTTT**AGCT**GTGTTTCATTGCTCA
 ATAATAAGCCTGAATTCATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGGK
WSDEACRSSKRYICEFTIPK

094199-08301

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTGCA
GCTCCGCTGCTGCTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACC CGCAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCTTCCCCGCGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

094192.08204

290/330

FIGURE 290

MKLAALLGLCVALSCESSAAFLVGSAKPVAQFVAALESAAEAGAGTIANPLGTNLNPLKLLLS
SLGIPVNHLEGSQKCVaelGPQAVGAVKALKALLGALTvFG

0941992.082801

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGACAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGACGCCGATCACATGAAGGTGGTGCCAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGCCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACAG
 CCCGGGCTCCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGGCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAAACAAGAGACTCGGGGGAAAATTCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAATTAATTCTTGTTGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCGAAGTCGACACTTTCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCTCCACCTTTGACAAGAA
 TTTTCGTTGTATGTCTCAAAC TGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC
 TGCTTATTCATGCCCTCCTGTATCAAGTGGACCGGCCATTTTCATTTATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGCAGGGTGGTGAATCCGACTCTCCTATAAATTTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTCTTTGTTCTTAACTAGTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTTACACATACATACCTATGAT
 AAAGTTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAAC TATTATAGAGAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCACCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATGAAGGGAGGACTACTACAAA
 GCATTAATTTGATACATATTTTTTAAAAAAGGAAAAAAGGAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATG**AG
 GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
 CACCCAAAGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
 GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
 TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCCA
 TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCTGAGTCCC
 GAGCCCACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
 CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
 TCTACCACCCCCAG**TAG**GGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGG
 CTGTTGGGACTGGGACCCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
 AAAAAAAAAAAAAAAAAA

00449-13304
 10020-2646

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMFNHQVLLGPEEDQDHIYHPQ

0994193.082801

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACTGCGGGATT
 TGTTCAGTTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
 CCCCAGCAGTGTGGAGATTTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATAACAACAACACAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATCTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCCTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAGAAGCTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAAGTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAAACAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

CAGCGGGGTCCCAAGCTTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
TCGCGGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCCATGCGACCCGTGTGGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCGCTGCTGCTGCTGGC
GCAGCTGTCAGACGCCGCCAAGAATTTTCAGGATGTGAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAAATTTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACACGATGTGCTAGCCCCGCTCCCGCAGTCGAGCCAAAGCTGTGAACAAGGTAG
AATATGCACAGCAGCGCTGSAAGCTTCAAGTCCAAGCAGCAGCAAGTCTGTCTTTGACCGG
CATGTTGTCTCTCAGCTAAATTTGGGAATTTGAATTCAAAGTGACTAGAAAGAAACAGGCAGACAA
CTGTTGAAGAAGTACTGGGTTTGTCTGGGTTTCAATTTAATACCTTGTGTATTTCACCAACT
GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTTTTCTGTGTAACGTA
ATAATAGAGACATTTTTAAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
AACAACCTTTTTTCAAGTCACTTTACTAAACAAACCTTTGTAAATAGACCTTACCTTCTATTG
TCGAGTTTCATTTATATTTTGAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTTCATGGTAAACGGGAT
CTAAATAGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
CAATGCATCCTAGAACAAACTGGCCATTTGCTAGTTTACTCTAAAGCAATAACATAGTCTTG
GTGTTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCTAAGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAACCCAGCCTCCCTGGATGTGATAATATATACACATTTG
TCAGCATTAAGGCTGTGTTGAGAGGCAGCTGTTTTCGAGCTCCAATATGTGCAGCTTTGAACT
AGGGCTGGGGGTGTGGGTGCCTTCTTGAAGGTCCTAACCATTTATTGGATAAAGCTGGCTTTTT
TCTTCTATGTCTCTCTTTGGAATGTAAACAATAAAAAATAATTTTTGAAACATCAA

300/330

FIGURE 300

MATLWGGLRLRGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVYLT
VEFILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

0941902-02204

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCAATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTCCAGAGGTCTCACCTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCATGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTGTTTTGCCCCAAAATTCACAACTAACAAGGCAGAAGTACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

0944392.03201

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYIILFKVSRIILI
ILHQ

00941992-002601

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCATGTTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
TGGATTATTCTTGGGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTCCAGGAGAGCAGCCAAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCATTATGGGCGCTTCCAGAACCCTGACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCAAAGGA
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATGTGTCTGCATGTGAGCCCGAAGAGCCTCGAACAACCTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGTATATTGATCGTGAAGAAGACCTGTGGAAATAA
GAGTTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAATAATCAGAGGCCACCTACATGACCATGCA
CCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAAGTGGGG
GAATGCCAAAAACACAGCAGCCTTTTGAGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGCTGCTGGGCCACTCTACCACTGATTTCAGACTCCCGCTCTC
CCAGCTGTCCCTCCTGTCTCATTGTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCTCAAACCCCCGTT
GGATCAGACCCCTCTGTGGGCGAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCAATCA

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

CTATGGAAGAAGCTTCC TGGAAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG
GTTCTACCTACTAAAGACAGGAAGATCATAAAGTACAGATACTGAAATGTAGAGTTGG
AAACTACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTA AAAGTACGGAACAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGCGGCTGGTGGCTCTGGGGATTGGTCTGTGATGCAGCGCAATTACCTACAAGA
TGAGAATGAAATTCGCACAGGAACCTCGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAGATCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTGTGGAAGA
TGGAAAAGGAAATATGAATGTGCTTATTTTCATAATGGGAAAATGCCACCTTACCTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAA

306/330

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFFRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

0991492-09901
109220-2091490

CCACACGCTCCGCGCAGTCGCGCAGTTCTGCTCCGCTGCCAGTCTCGCCCGCATCCCGC
CCCCGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGAGCCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCCTTTGCTGAAGCCCGAGTCCGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAAGCCAGAGAGGGGCGAGAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGCGCGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCGACAAGGCAAGACCACTGC
GACAAAAACAAGTTAAATGCTCTTTCCGGGTCAAACCTCTCGGCTCCAAGAAGAGCGCGAG
AAGAAGACAGAGCTTACGTTATAGGTTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
TCTGCAGCTGCAGGCCGATGGAACCATTTGATGGCACCAGAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATATTATTGTGACATATTATCATATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTGCGGTGCTGAACGGGAGGCAATACCTGAGCCACCAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGCGTGTGAACAGAACTTACCTCCAGGTGCTGTTGAAT
TCTTTAGCAGTCTCTTCAACCAAAAGCTTCAAAATTTGTGAGTGACATTTACCAACAACACGAG
CAGAGTCTCACTATTCTATTCGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVF SRVKLFSGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLG LNKKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSM SHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCC
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCCAG
 CGCGCTCCGGGCGCTGCCGGTTTGGGGGTGTCTCTCCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCAGCCCGGGGGCAGCCGGCCCGGTGTCCG
 CGCAGCGGCGGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGCGGCCCCGCGCGCCGGACCGCGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAATGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCC
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCCTGTACGCCCTCTGTCTCTACCGCCAGCGTCGTTCTGCGCGGGC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCCTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKSLCQQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACTCTT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDPSASRRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRRLR
RQDPQLKGIVTRLYCRQGYLYQMHPDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATTGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAAGGACGACGCTTTCCTCGGAACCGAACCGAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACCGAGGTAGACCCGCGGGGGTGTGTGTCTGACATAAATAAATAATCTTAAGACAGCTGTTCCC
 CTCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTCACAAGAAAAAGATGTGTCATTT
 TTCTCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAA
 AGAAGCTGGTGGTGGTGTTCCTTTCTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAACATCTGC
 AAAGAAATTTGAGAGAAGAAAGTTGACCGCGCGAGATTGAGGCATTGATTGGGGGAGAGAAACGAGCAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTTCTTAACCACCTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACAGATAAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTCTGCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCTGCAGCAACCAAGTTGACGAAGGTGATTTGTGTCGGAACCACTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGACACAGCTTCAAGCAGCTGAG
 GCATTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAATCTTTGACAATCGTCTTACTACCATCCGGAATGGAGCTTTTGTATACTGTCTAAA
 CTGAAGGAGCTCTGGTTCGCAAAACACCCCATGAAAGCATCCCTTCTATGCTTTTAAACAGAAATCCTTCTTT
 GCGCGCATAGACTTAGGGGAATTTGAAAGACTTTCATACATCTCAGAAGTGCCCTTTGAAGGCTCTGCCAAT
 TGAGGTATTTGAACTTGGCACTGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAC
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCTCATGACCTTCTACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACACCCCTTGGAACTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCGCGGTGTAACACTCCTCCCAATCTAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCAATGACACA
 TGGGGCGTACAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAATATGTAAGTCTGCAAGATA
 GAGCATGTACACATGTATGGTGAGTAAATCCGTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCA
 GCAACCACTACTCTTTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGCTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCAAGGTGCAGAGAGAAACCTTACCATCCAGTGACTGATATAAACAGTGGGATCCCGAATG
 GATGAGGTCTAGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTATGCGCTGCAGTGATGCT
 GGTCAATTTTCTACAAGATGAGGAAGCAGCACCATTGCGCAAAACCATCACGCCCCAACAGGAGCTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGGCCACTGCCCCATGCCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAATCTCCCTTCAACCAACACAAACAGTTAACACAATAAATTCATATACA
 CAGTTCAAGTGCATGAACGTTATTGATCGAATGAACCTAAAGACAATGTACAAGAGACTCAATCTAAACA
 TTTACAGAGTTTACAAAAAACAACATCAAAAAAAGACAGTTTATTAATAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTTCAAAAAAACAAGAAAGAAATTTATTTATTAATAAATCTTATTTG
 TGATCTAAAGGAGACAAAAA

094192.08201

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGISTNTRLLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRDLGELKRRLS
 YISEGAFEGLSNRLRYLNAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHHLHNPWNCNCIL
 WLSWWIKDMAPSNTACCARCNTFPNLKGRYIGELDQNYFTCYAPVIVEPPADLVNTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGN
 TTASATLVNTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGTPVVDWETTNVTTSLTPQ
 STRSTKTFITIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRRQN
 HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

CGCGCCGGGAGGCCATCTGCCCCACAGGGGACAGGGGCGCGGGGCGGGCTCCCGCCCGGCACGAT
GGCTTGCAGCGACCTTCGGCGGCACCCCGAGGGCGCGCCAGGCTCGCCCGAGTCCGTCCGTA
GGCGCCCGCGGCCCGCGGAGCAGCAACGACGCAACTGAGCGGGGAAGCGCCGCGGCTCCGGGATG
GGCATGTCCCTCTCTCTCTCTCTCTTGTCTTGTCTTCTTACTGTTGGAACCTTGGGGATCA
CACTTGAGATCAAGAGAGTGGCAGGAAAAGGTCACTTGGCTCGCCACCATCAACTGAAGGCG
TTCCAGAAAAAGACATCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTATCGATCGTCTATGTCTACAATACTTGCATGAGGACAGGAAGGGCCCG
AGTGGCTTTTGCTTCCAATTCTGCGAGGAGATGCTCTTTCAGATTGAACCTTCTGAAGG
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACAGTGTGGAGCCAT
GTCATCTTTAAAGTCTTTAGTGACACCATCAAGCCCAAGTGTGAGTTGAGGAGAGAGCTGAC
AGAAGGAAGTGAAGCTGATTTGCACTGTGAGTCACTCTCTGCGACAGAGCCCAATTGTGTATT
ACTGGACCGCAATTCGAGAGAAAGAGGGAGGAGGATGAACCTCTGCCCTCCAAATCTAGGATT
GACTACAAACCCCTGGACGAGTTCTGCTGCAAGTCTTACCATGTCTCTTCTGAGCTGTA
CCAGTGCACAGCGAGGCAACGAAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTGTACAGT
ATGTACAAGACATCGGCATGTGTGACGAGGACGTGACAGGCATATGAGCTTGGAGCCCTGTGT
ATTTTCTCTTGGTGTGGCTGCTAATTCCGAAGGAAGACAAGAAGATATGAGGAAGGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGCTCTTGTGAACAACCGACT
CCTCTTCTCTCAGGCTCTCGGAGCTCAGCGTCTGGTTCTTCTCTCCTCGCTCCACAGCAAT
AGTGCCTCAGCGACGCCAGCGAGCACTGTCAACTGACGACGACCCAGCCAGGGCTGGCCAC
CCAGGCATCAAGCAAGCTAGTGGGGCCAGAGTGTGAGAGTCTGTGAACCAAGAAAGATGCCACCT
CTAATCTGACAAAGCAGGAAACCAACACCCAGCATGATGCCAGCCAGAGCAGAGCTTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCCACGGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCAATTGAGCTTCAAGTCAAGCCACGACCAACACAGATGAGAGGTCATCTTAAGTAGCA
GTGAGCATTTGACGGAACGACATTTCAGATGAGCAATTTCCCTATACCAATACCAACAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACGACGATGAAGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAAGGACCTGTGGTGAGAAGTTGGGGAAGGTG
AGGTGAATATACCTAAAATTTTAATGGGGATATTTGTATCAGTGCTTTGATTACAATTT
TTCAGAGGAAATGGGATGCTGTTTGTAAATTTTTCATGCAATTTCTGCAAACTTATTGGATT
ATTAGTTATTACAGAGTCAACGAGAACCCACAGCCTTATTACACTGTCTACACCTGTAC
TGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAAACATGTCTCTTCTTCTGACTTAAC
TTCAATTTGTCAATAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTGATTGAGCCCAAAATTAAC
TATGAAGGAGACAAAATTTGTGAGAAAGGATTTGGAAGACTTCTCACTCTTCATGTGTT
ATGAGGATTGTTGACAAATTAGAATAATATAATGAGCAATTGTGGATTTCCCTCAAAAT
CAGATGCCCTCAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCAATT
TATCAAGCTCTTTAGAAGAAATTTCTTACAGAAAAAGGGAATCTAGAATGCTGAAGAGATA
CCCAACATCATCTATAGTCTCTCTTCTTCTTCTGAGAAAAATGTGAACCAAGAAATGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAATCCAGCAGGTGGAGGTTGCAGTGTAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGACGGGAGCTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYVGTLTGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCGCGCGCCACGGCACGGCAGCCA
 CCATGGCGGCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCCGCCAGAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAACTGCCATCTGCCATGCAAAATTTACGGCTAGTCCCGAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGCTGGATCAAGTGATATTTTAT
 ATTTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAGGCGGAGTACATTTTACGACTAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTAAACGAATTTACAAGTGCAGATATGGCACATATCAGTGCAAAAGTGAA
 AAAAGCTCCTGGTGTTGCAAAATGAAGATTCATCTGGTAGTCTTGTTAAAGCCTTCAGGTGCGAGATCTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCCATCTCCATTACAG
 TATGAGTGGCAAAATTTGTCTGACTCACAGAAAATGCCCACTTCATGGTTAGCAGAAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTTGTGCGCTAAACGTTGTCCCTCCTCAAAATAAGCTGGACTAATTTGACGAGGCCATATATAGGAAT
 TTGCTTGCTCTAGCGCTCATTTGGTCTTATCATCTTTGCTGTCTGTAAGGCGCAGAGAAGAAAAATATGAAAA
 GGAAGTTCATCAGCATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCACCTGCCAGAAGCTACATCG
 GCAGTAATCATTATCCTCGGGGTCATGTCTCCTTCCAACATGGAAGGATATTTCCAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCTTTACAA
 GACTGATGGAATTACAGTTGATATAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAGGCACAGAGATTAGAGCAGCTGTAAGAACAC
 ATCTACTTTTATGCAATGGCATTAGACATGTAAGTCAGATGTATGTCAAAATTAGTACGAGCCAATTTCTTTGT
 TAAAAAACCCATATGATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATAACTACCACTAACAA
 ATTTTAACTTTTTCATATGATATTTCTGATATGTGGTCTTTTAGGAAAAGTAGGTTAATAGTTGATTTTTTCAA
 AGGAATTTTAAAAATTTCTACGTTCTGTTTAAATGTTTTGCTATTAGTTAAATACATTGAAGGGAATACCCG
 TTCTTTTCCCTTTTATGCAACACACAGAACACGCGTTGTCTGCTCAAACATTTTTTATTGCAACTACA
 TGATTTCAACAATCTTCTTAAACAACGACATAAAATAGATTTTCTGTATATAAATACTTACATACGCTCCA
 TAAAGTAAATTTCTCAAAAGTGCATAGAACAAATCGTCCACTTCTACAGTGTCTCTCGTATCCACAGAGTTGATGC
 ACAATATAATAACTCAAGTCCAATATAAAAACTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACTA
 TATCAATATCAAAATGCATATATTTTAAAGAAAGATTATCTCAATAACTCTATAAAAAATAAGTTTGTATGG
 TTGGCCCATCTCAACTCTCACTACTATTAGTAAGAACITTTAACTTTTAACTGTAGTAAGGTTTATTCTACGTT
 TTTCTCAACATGACACCAACCAATCAAAACGAAGTTTACTGAGGTCTAACATGTGAGGATTAAATCCAGTAT
 TCCGGTCACATGCATTCCAGGAGGAGGTACCCATGTCACTGGAATTGGGCGATATGGTTTATTTTCTTCCC
 TGATTTGGATAACCAAAATGGAACAGGAGGAGGATAGTGATTCTGATGCCATTTCCCTCGATACATTTCCGCGCT
 TTTTCTGGGCAAGGGTGCCACATTTGGAAGAGGTGGAATAATAAGTTCTGAAATCTGTAGGGAAGAGACACAT
 TAAGTTAATTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATATAAAGACAAAGTTACCCACAACT
 GAGATCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAARAACTCATGTGTAATGCGGTATAA
 TGTATAACAGGTGACCAATGTTTCTGAATGCATAAAGAAATGAATAAACTCAACACAGTACTTCTTAACAA
 CTTCAACCAAAAAAGACAAAAACATGGAACGAATGGAAGCTTGTAAGGACATCTGTTTGTAGTCCAGTGGTTT
 CCACAGCTGGCTAAGCGAGGAGTCACTTGAGGCTTTTTAAATACAAACATTTGGAGCTGGAGGCCATTATPCTT
 AGCAAACTAATGCAGAAACAGAAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAAATGATAAGACT
 TATGAAACACAAAGGAGGAAACAAATAGACATTGGAGTCTATTGTAGAGGGGAGGGTGGGAGAGGAAAGGACGA
 GAAAGATATACTATTGATGACTGCTTTCACACCTGGGTGATGAATAATATGTGTAACAAATCCCTCTGACACA
 TGTTTACCTATGGAACAAACCTCATGTGTATCCCTAAACCTAAATATAAGTTAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTGTGCTCCCTTGCTGGGTTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACATTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCACAACAT
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGCGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC
 TCTGATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCAATTTCA
 AACAGTCTCCCTTCCATGTGTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTTC
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCACACTCGCCAGCTACCCCATCATCCCTTCCCTTGGTGCCCTCCTTTTTTTTTT
 TATCTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

0000000000000000

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGCGGTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGCCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA .

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACGACCTC
 GGTTCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACCGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAACTGCAGGTTCACACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
 CCCATACCACGGCGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCGTAACGT
 GCTGAAGCCCCGGGCCCCGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCAGCG
 CCAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTTCATCTAGGGTCTG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGAAAAGGTACCCGCGAGAGACAGCAGCAGTCTGTGTGGAGCAGCGGTGGCCGGCTAGGAT
GGTGTTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGACAGACAGACTGCGATGACAAAGGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAGCTCAAACGCTGAGCGTGTAG
ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGGCCAA
GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGG
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
ACAGTTACAGACATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCCCTTGCACCCGA
TGACAGCTCTGAAGAGGCAAAGACACTCAAAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCAACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
GGTCCCCGGGATCTGATGTCTACTTCTCTCGTGAAGCCCTGGTGACTGTCAACAAATCGAG
GTTATTAATTGCAGATCACAGAAATAGAAACAACAACTTCAGCATCCCTGAGGGCTTCAGAG
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCTCTGTCACCTCGATCCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCGTGTC
ACAGCCGGCACCAAGAGTACGTGCACTCATGCCAGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAGTACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACAGAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCACACAGCAGGGACCCCT
CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
GATCACAACTCAGCGAAGACCAGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGAGCTGAGTGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGAGGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
GGCCCCACCCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCCAACCCAGATGTGGCAACAGGACCCCTCGCTCATACCTCAC
CGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCCAAGAGTGTCTCTGGACTACCTTGG
CATAGTTCGTGTTTCAGTAAGAGGAGACCTGATCACCATCTGTGTGCTTCCATCCTGCA
TTAAATTCCTCAGTGTGGCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSFNFVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAIFDTLCTDDSSEEAKLTMDILTAAHTSTEAKGLSSESSASSDGPHPV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSIVETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFPTSETPTMDIATKGFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CTTTGACCTTTGAAGACCAAAACTAACTGAAATTTAAATATGTTCTTCGCGGGAGAAAGGAG
 CTTGACTTACACTTTGGTAATAAATTTGCTTCTTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACACGCA
 AAAGGACTTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAATTTTCAACAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAAATGTGAGTGCGCTCCAGCTACGGTGCGAGTTGCTTTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCTCCCACGACCTCATTTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATG
 GCTACAACAGCAGTTTCTGACTACCACCTTTAGGCACCTACGGACTCGAAGGCGAGCTTAGA
 AACCATAACGTTTACAGAAATCTCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAACTAGTACGGCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCCGAATCACTCCGAGGAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCATT
 TAGTAACCCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGTTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGACAGTGCAGTACGACGATCTCGGCTCTCACCGCAACCTCCGCTC
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTGGGTGATTTTTGTATTTTATGAGAGACGGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACTCTGACCTAGTGATCCACCTCTCGGCCCTCCAAAAGTGCTGGGATTACAGG
 CATGAGCCACCAAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGAAATGAAGT
 GGAACCAAAATAGGTAAATTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAAATGCCATATAAATTTCAAATTTCACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATCACATTCTTGGTTCAGATAAAATCAAC
 TGTTTTATATCAATTTCTAATGGATTTGCTTTCTTTTATATGGATTCTTTTAAACTTATT
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAATCTTTGTACTCAA

09941992-032804

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKRTARQPNCYLFFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHL LPENV SALPATVAVASPH TTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFOAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPF EKWLLIGSLLFGVLFVLVIGLVLLGRILSES LR RKYSRLDY LINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCCA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAATCAGCGGTTTCAAGGGGACACTGTGT
 CCTCGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGCT
 GGGATCCTCTTCTCTCGGTGCTCTGGCACCATTATGCAGAAGAAGAGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTCACCCGTGAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAACCGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCCTGCTGTCTCCCTCCCTCCCTTCTCCAC
 CTTCAGCCTCTGGCTACAACACGCTGACGCCAAGGCAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGCAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCAGCTCTCTCTGACAGGAGCTCCCGCCCCCATGCGAG
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTGAGC
 CGCAGGCCCTGATCGCCTTCTGAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTCTGGCTCTCAGCTTGACTCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGT**TAG**GGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 AACAGCATGATCTGGCTGGATCAGCACCATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCCGAGCTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTGACCCCTGGAGCCACAGCGGCTGGCCCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTATGCCAGTGTGCGACCCTGCCTTCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCTAGACTTAGTCCCAGGCTCTCTGCTCAGCTGGTGATGAAGAGGAGCAGTGT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAAGGAAGCCT
 GTGAAAACGTGATTCTGGGCCCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGACTGTCGCACCTTGAGTTTGAGGGCCAGTGGGCCTG
 ATGAACGCTCACACCCTTCAGCTTAGAGTCTGCATTTGGCGTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACAGATCCACGTGGGGACTCCCTGAGGCCCTGTAAAG
 TCCAGGCCCTTGGTCAGGTGAGTGACATTGCAGGATAAGCCAGGACCCGCACAGAAGTGG
 TTGCTTTTNCATTTGGCCTCCCTGGNCCATGCCTTCTTGGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCCATGGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGTGTCTAACACAGAGGAGTAGGAAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACACTACTATTTTTTTTCTTTTCCATTATTTGTTTAAAGACAGAATCTCTGTGCT
 GCTGCCACGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGCACCACACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGTGGTCTTGAACCTCTGAC
 CTCAAATGAGCTCCTGCTTCAGTCTCCCAATTGCCGGGATTACGGCATGAGCCACTGTG
 TCTGGCCATTTTCTTTTAAAAAGTGAATTAAGAGTTGTTTCAATGCAAACTTGGAAAG
 ATGGAGGAGAAAAGAAAAGGAAAGAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
 TATTTCGTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTATCTGTATATACAACCTTGTATCTCGCCTTTTCCACCTATCTGTTCC
 ATCACTTTATCCAGACTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTCACTCA
 GCTGCATAAAAAAAAAAAAA

00000000000000000000000000000000

[illegible][illegible][illegible][illegible]

06-07

06-08-2019

[illegible][illegible][illegible]

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000

00000000000000000000000000000000